

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

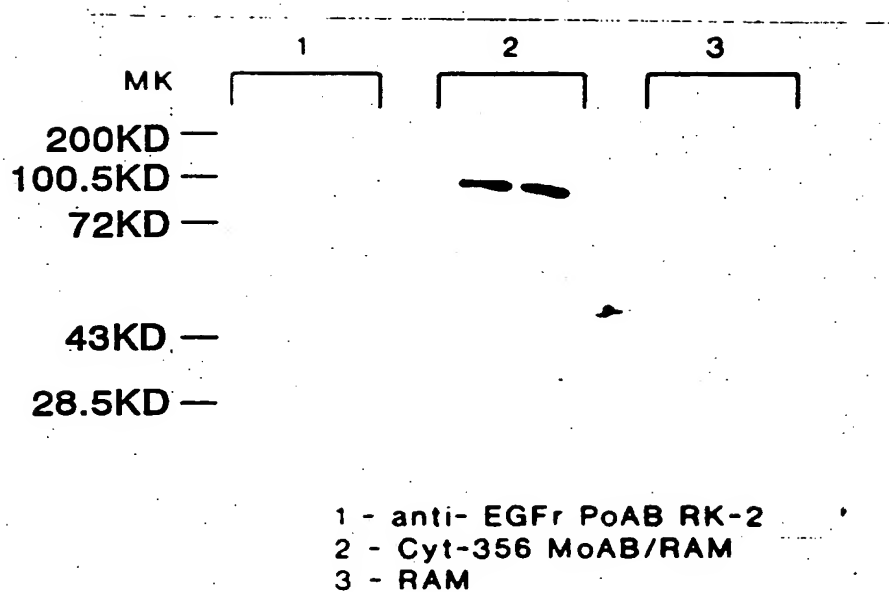
- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

1/130

FIGURE 1



2/130

FIGURE 2B



FIGURE 2A

FIGURE 2D



FIGURE 2C

3/130

FIGURE 3B



FIGURE 3A



FIGURE 3D

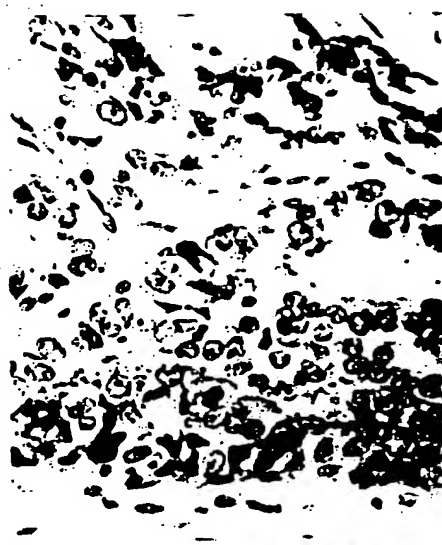
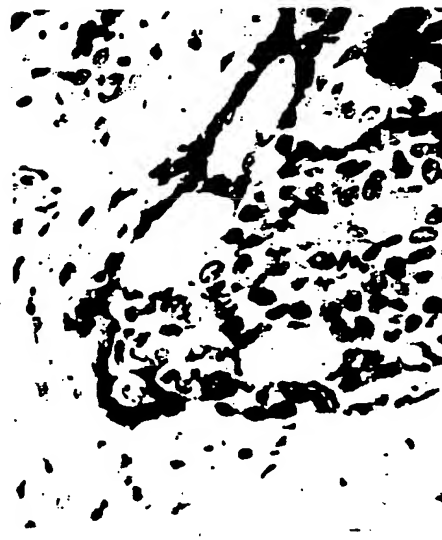
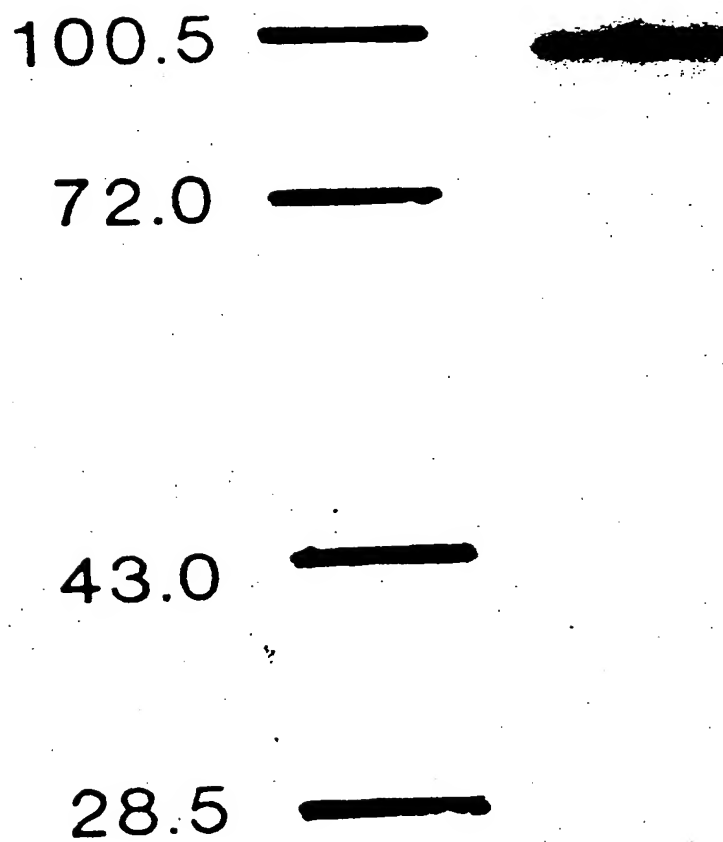


FIGURE 3C



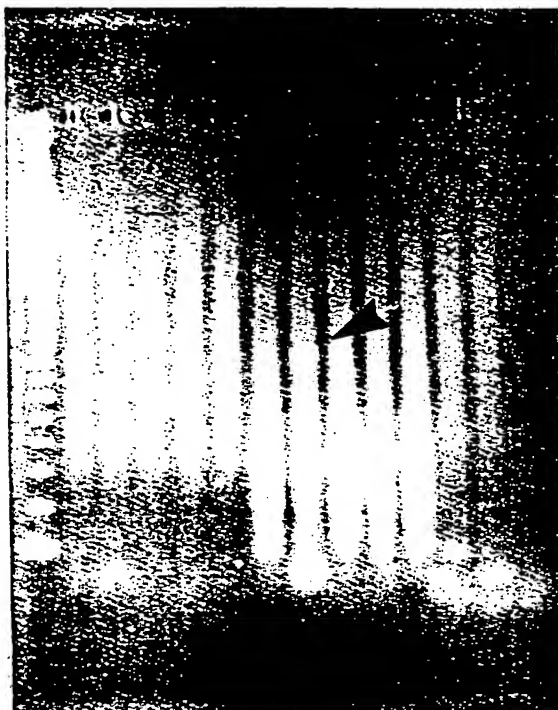
4/130

FIGURE 4



5/130

FIGURE 5



6/130

FIGURE 6A

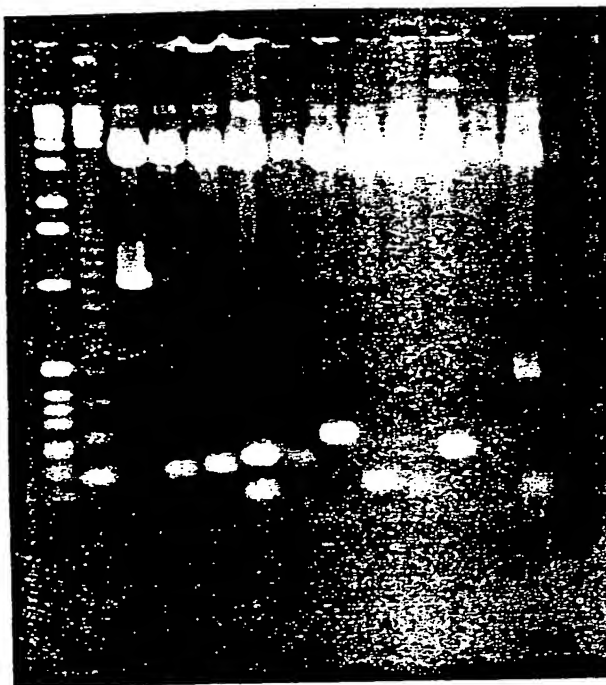
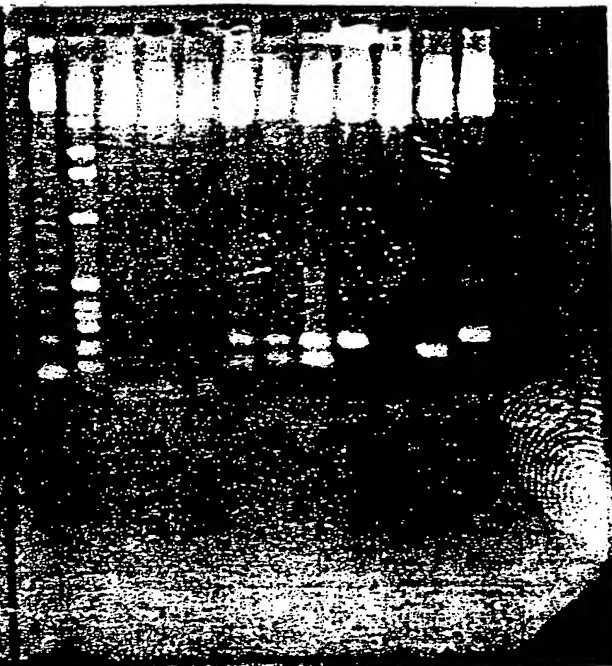
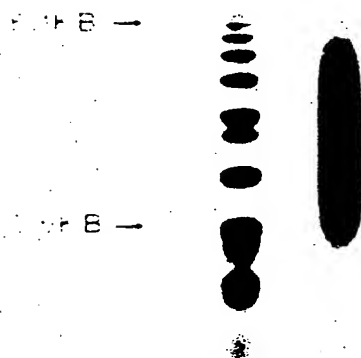


FIGURE 6B



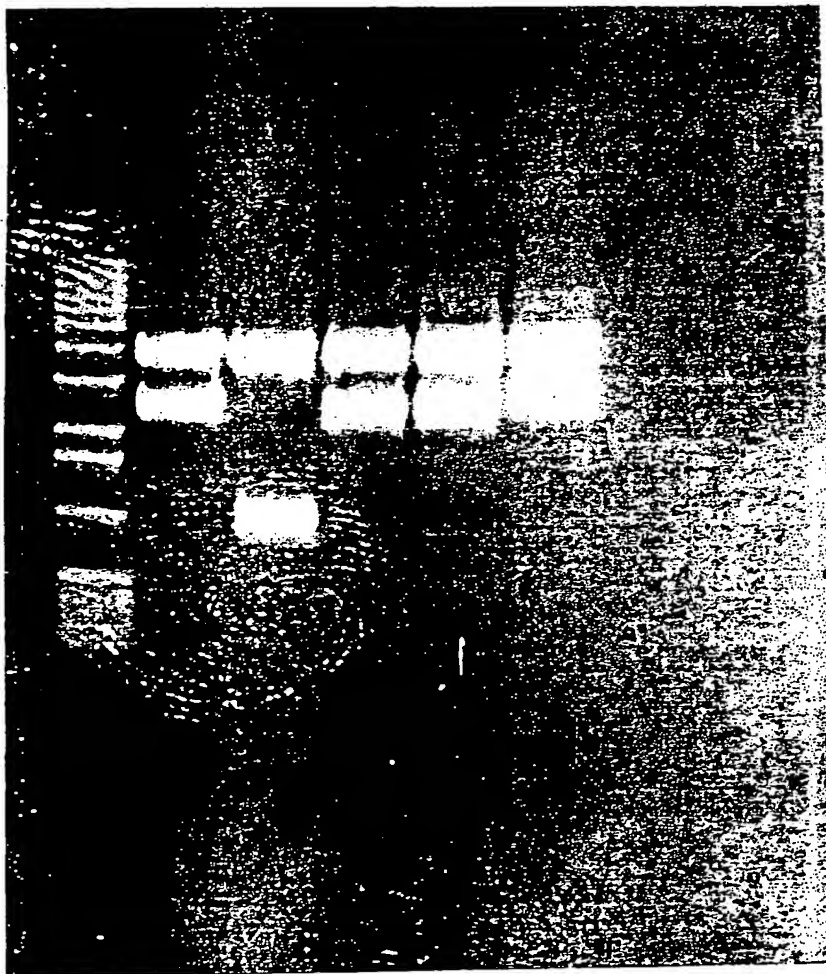
7/130

FIGURE 7



8/130

FIGURE 8



9/130

FIGURE 9

4—
3—
2—
1.6—

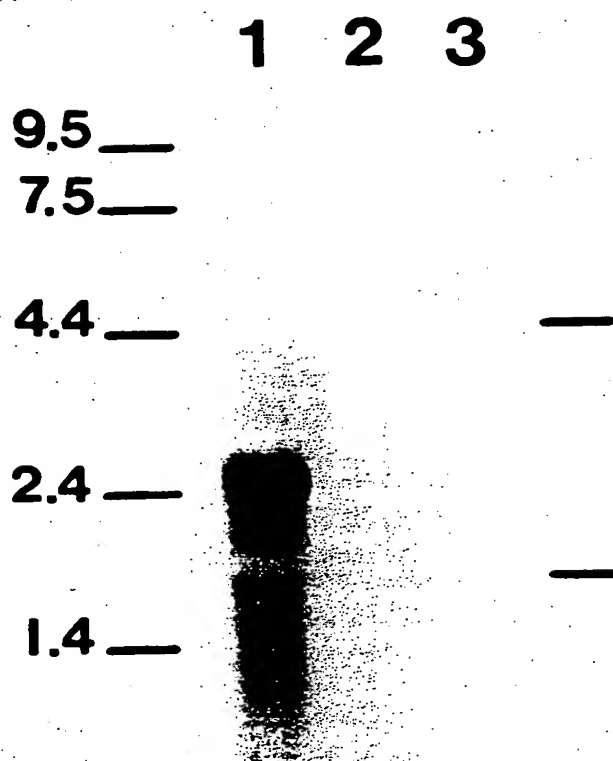
10/130

FIGURE 10



11/130

FIGURE 11



12/130

FIGURE 12A

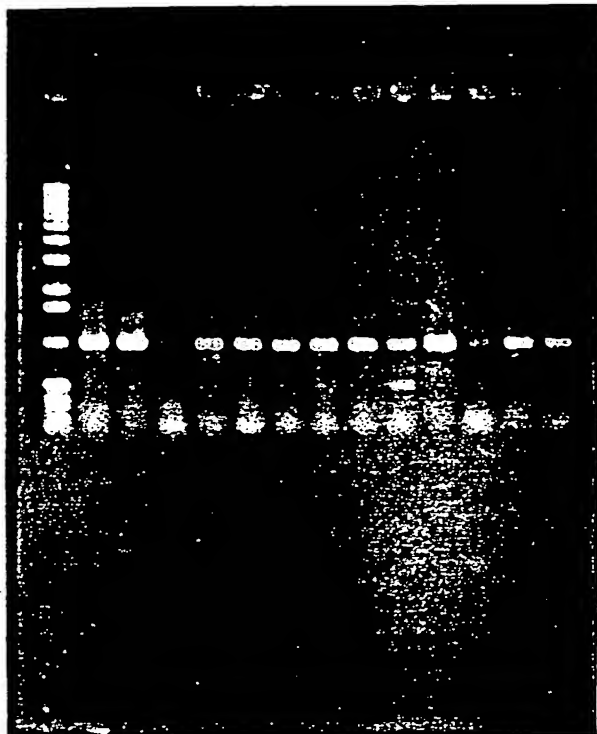
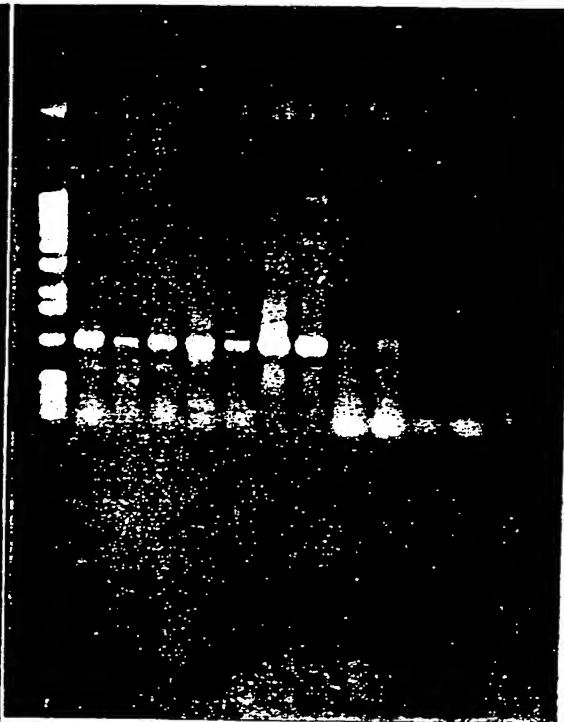
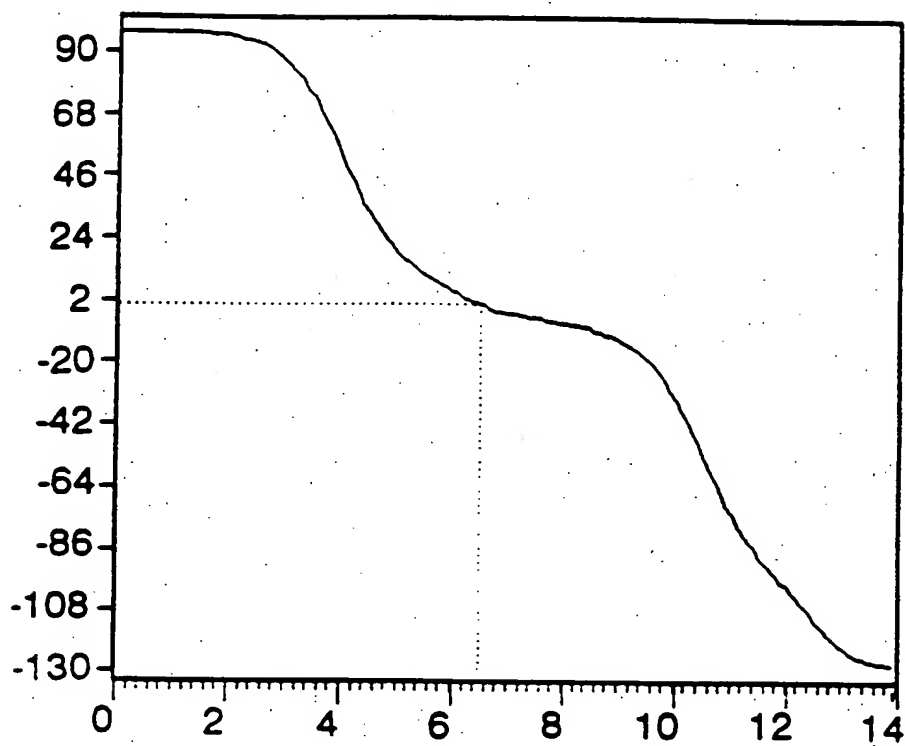


FIGURE 12B



13/130

FIGURE 13



17/130

FIGURE 14-4

Semi-graphical output.

=====

Symbols used in the semi-graphical representation:

Helical conformation: X Extended conformation: -
 Turn conformation: > Coil conformation: *

10 20 30 40 50
 | | | | |
 MWNLLHETDSA V A T A R R P R W L C A G A L V L A G G F L L G F L F G W F I K S S N E A T

XXXXXXXXXXXXXXXXX--->>-----XXXXXXXXXXXXXXXXX
 XXXXXXXXXXXXXXXXXXXX--->>-----XXXXXXXXXXXXXXXXX

60 70 80 90 100
 | | | | |
 N I T P K H N M K A F L D E L K A E N I K K F L Y N F T Q I P H L A G T E Q N F Q L A K Q I Q S Q W

18/130

FIGURE 14-5

XXXXXXXXXXXXXXXXXX-->>-----*****XXXXXXXXXX-X*--
XXXXXXXXXXXXXXXXXX-->>-----*****XXXXXXXXXX-X*--

110 120 130 140 150
| | | | |
KEFGDVELAHYDVLLSYPNKTHPNYISINEDGNEIFNTSLFEPPPG

-->>*****-->>-->>----->>***X----->>***>>
-->>*****-->>-->>----->>***X----->>***>>

160 170 180 190 200
| | | | |
YENVSDIVPPFSAFSPQGMPEGLVYVNVARTEDFFKLERDMKINCSGKI

21/130

FIGURE 14-8

LYHSVYETVELVEKFDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY

-----XXXXXXXXXXXXX-X-----XXXXXXXX----->XXX
 -----XXXXXXXXXXXXX-X-----XXXXXXXX----->XXX

610 620 630 640 650
 | | | | |
 AVVLRKYADKIYSISMKHPQEMKTYSVSFDLSFAVKNFTEIASKFSERL

XXXXXXXXXX-----X*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX
 XXXXXXXXXXXX-----X*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX

660 670 680 690 700
 | | | | |
 QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY

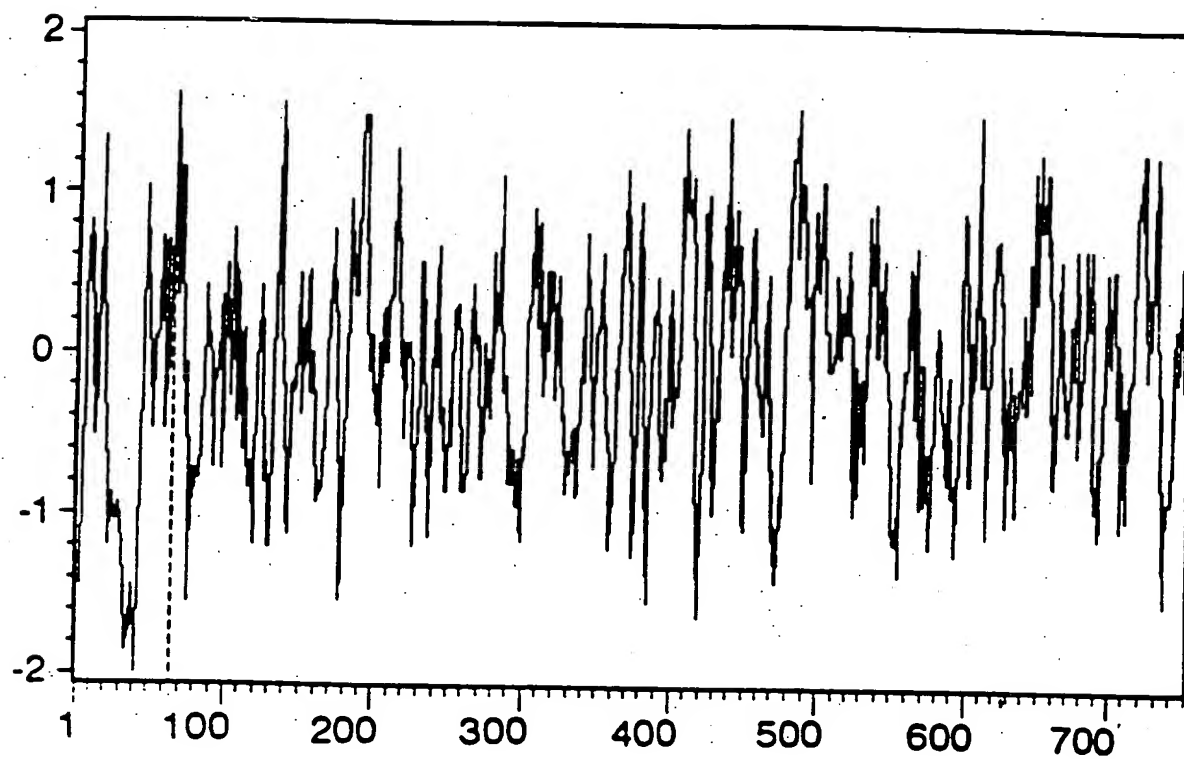
XX>>>***-----XXXXXXXXXX-->>***>----->***>
 XX>>>***-----XXXXXXXXXX-->>***>----->***>

710 720 730 740 750
 | | | | |
 AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAETLSEVA

----->--XXXXXXXXXX**XXXXXXXXX-----XXXXXXXXXXXXXXXXXX
 ----->--XXXXXXXXXX**XXXXXXXXX-----XXXXXXXXXXXXXXXXXX

22/130

FIGURE 15A



23/130

FIGURE 15B

* * * * *
 * PREDICTION OF ANTIGENIC DETERMINANTS *
 * * * * *

Done on sequence PMSANTIGEN.

Total number of residues is: 750.

Analysis done on the complete sequence.

The method used is that of Hopp and Woods.

The averaging group length is: 6 amino acids.

-> This is the value recommended by the authors <-

The three highest points of hydrophilicity are:

(1) Ah= 1.62 : From 63 to 68 : Asp-Glu-Leu-Lys-Ala-Glu
 (2) Ah= 1.57 : From 132 to 137 : Asn-Glu-Asp-Gly-Asn-Glu
 (3) Ah= 1.55 : From 482 to 487 : Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third points gave a proportion of 33% of incorrect predictions.

FIGURE 16-1

The best scores are:

The best scores are:		initn	initl	opt
CHKTFER	G.gallus mRNA for transferrin receptor	203	120	321
RATTRFR	Rat transferrin receptor mRNA, 3' end.	164	164	311
HUMTFRR	Human transferrin receptor mRNA, complete cd	145	145	266

Gene	Accession	Length (nt)	Identity (%)	Overlap (nt)
CHKTFER	G.gallus mRNA for transferrin receptor	203	120	321
	51.9% identity in 717 nt overlap			

```

1020      1030      1040      1050      1060      1070
pmsgen  TGTCCAGCGTGGAATATCCTAAATCTGAATGGTGCAGGAGACCCCTCTCACACCAGGTTA

          ::      :      ::      ::      ::      ::      :
CHKTFE  TACACTTATCCCATTCGGGACATGCCCCACCTTGGAACTGGAGACCCCTTACACCCAGGCTT
          990      1000      1010      1020      1030      1040

```

```

1080      1090      1100      1110      1120      1130
pmsgen  CCCAGCAAATGAATATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTAT
        :::      :      :      :      :      :      :      :      :
CHKTFE  CCCTTCGTTCAACCAACCCCA---GTTTCCACCAGTTGAATCTTCAGGACTACCCACAT
        1050      1060      1070      1080      1090      1100

```

```

1140      1150      1160      1170      1180      1190
pmsgen  TCCTGTTCATCCAATTGGATACTATGACACAGAAGCTCCTAGAAAAAAATGGGTGGCTC
      : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE  TGCTGTTCAGACCATTCTAGCAGTGCAGCAGCCAGGCTGTTTCCAGCAAAAAATGGATGGAGA
      1110      1120      1130      1140      1150      1160

```


FIGURE 16-8

	1730	1740	1750	1760	1770	
pmsgen	GCTTTGAAGGCAAAATCTCTTAT-GAA-----AGTTGGACTAAAAAAGTCCTTCCCCCAG					
RATTRF	---TTGATGGAAAATA TCTATATCGAAACAGTAATTGGATTAGCAA AATTGAGGAACTTT 1140 1150 1160 1170 1180 1190					
	1780	1790	1800	1810	1820	1830
pmsgen	AGTTCAGTGGCATGCCCCAGGATAAGCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCT					
RATTRF	CCTTGGACAA TGCTGCATTCCCCTTTCTTG CATATTCAGGAATCCCAGCAGTTTCTTTCT 1200 1210 1220 1230 1240 1250					

FIGURE 16-9

HUMTFRR Human transferrin receptor mRNA, complete cd 145 145 266
54.3% identity in 464 nt overlap

	1230	1240	1250	1260	1270
pmsgen	AGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTAC-TGGAAACTTTTCTACAC				
			:	:	:
			:	:	:
HUMTFR	TATGGAAGGAGACTGTCCCTCTGACTGGAAAACAGACTCTACATGTAGGATGGTAACCTC				
	1140	1150	1160	1170	1180
					1190

```

1280      1290      1300      1310      1320      1330
pmsgen AAAAAGTCAAGATGCACATC-CACTCT-ACCAATG-----AAGTGACAAGAAATTACAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HUMTFR AGAAAGCAAGAAATGTGAAGCTCACTGTGAGCAATGTGCTGAAAGAGATAAAAAATTCTTAA
1200      1210      1220      1230      1240      1250

```

	1340	1350	1360	1370	1380	1390
pmsg n	TGTGATAGGTACTCTCAGAGGACGAGTGGAAACCAGACAGATA	TGTCATTCTGGGAGGTCA				
	:	:	:	:	:	:
HUMTFR	CATCTTTGGAGTTATTAAGGCTTTGTAGAACCAGATCACTATGTTGTAGTTGGGCCCA					
	1260	1270	1280	1290	1300	1310

	1400	1410	1420	1430	1440	1450
pmsgen	CCGGACTCATGGGTGTTGGTGGTATTGACCCCTCAGAGT-GGAGCAGCTGTGTGTTTCATG					
	: :					
HUMTFR	GAGAGATGCATGGGGCCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTTCCTATTGA					
	1320	1330	1340	1350	1360	1370

33/130

FIGURE 16-10

```
1460      1470      1480      1490      1500
pmsgen AAATTG---TGAGGAGCTTTGGAACACTGAAAGGAGGTTGAGACCTAGAAGAACAA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
HUMTFR AACTTGCCAGATGTTCTCAGATATGGTCTTAAAGATGGGTTTCAGCCAGCAGCAAGCA
1380      1390      1400      1410      1420      1430

1510      1520      1530      1540      1550      1560
pmsgen TTTTGTTCAGAGCTGGGATGCAGAGAAATT'TGGTCTTCTTGGTCTACTGAGTGGGCAG
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
HUMTFR TTATCTTTGCCAGTTGGAGTGGGAGACTTTGGATCGGTTGGTGCCACTGAATGGCTAG
1440      1450      1460      1470      1480      1490

1570      1580      1590      1600      1610      1620
pmsgen A-GGAGAAATTCAGAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
HUMTFR AGGGATACCTTTTCGTC-CCTGCATTTAAAGGCTTTCACCTTATATTAATCTGGATAAAGCG
1500      1510      1520      1530      1540      1550

1630      1640      1650      1660      1670      1680
pmsgen ATAGAAGGAAACTACACTCTGAGAGTTGATGTACACCGCTGATGTACA-GCTTGGT-AC
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
HUMTFR GTTCTTGGTACCAGCAACTTCAAGGTTTCTGCCAGCCCACTGTTGTATACCGCTTATTGAG
1560      1570      1580      1590      1600      1610
```

34/130

FIGURE 16-11

1690	1700	1710	1720	1730	1740
pmsgen	ACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGCAAAATCTCTTTATG				
:	:	:	:	:	:
HUMTFR	AAAACAATGCAGAAATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC				
1620	1630	1640	1650	1660	1670

35/130

FIGURE 17A

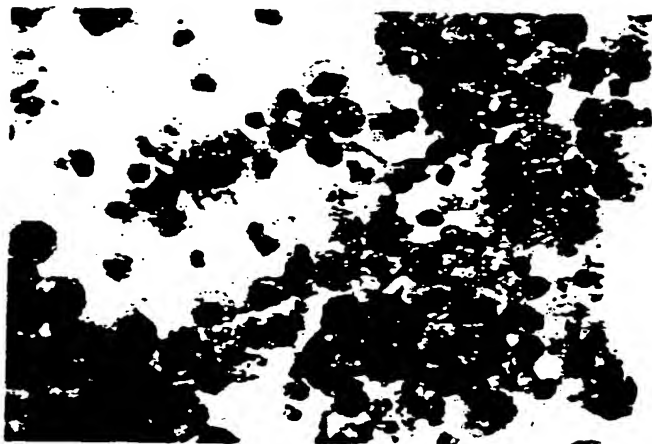


FIGURE 17B

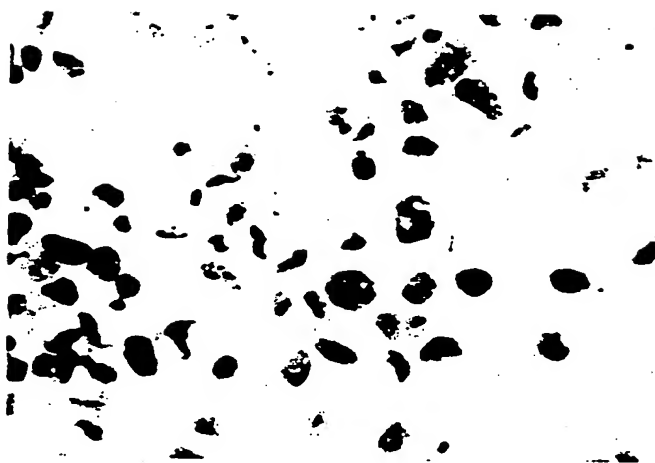
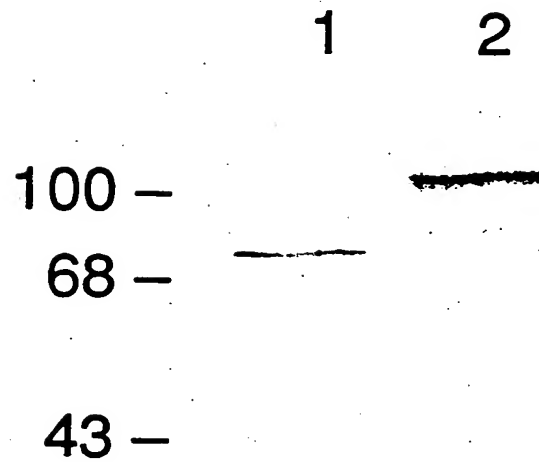


FIGURE 17C



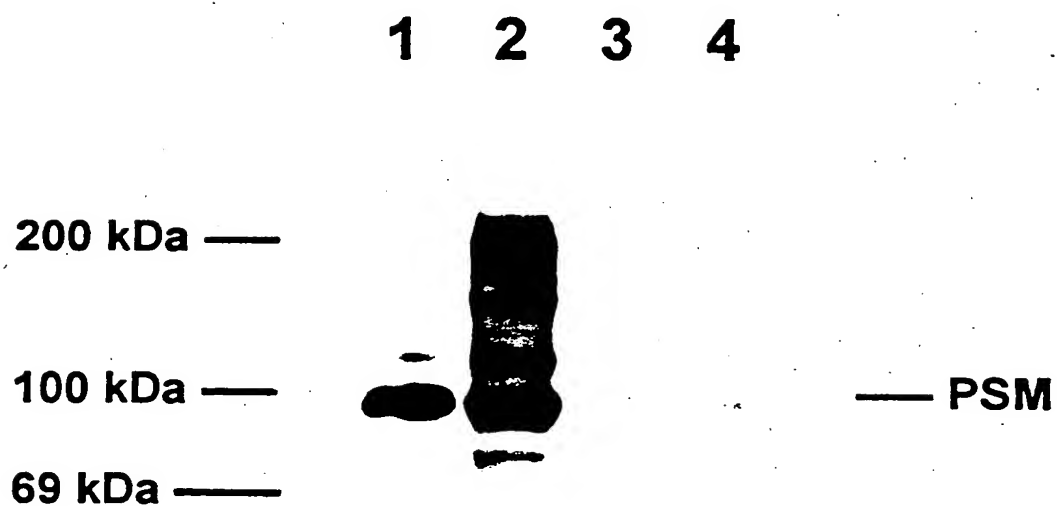
36/130

FIGURE 18



37/130

FIGURE 19



38/130

FIGURE 20

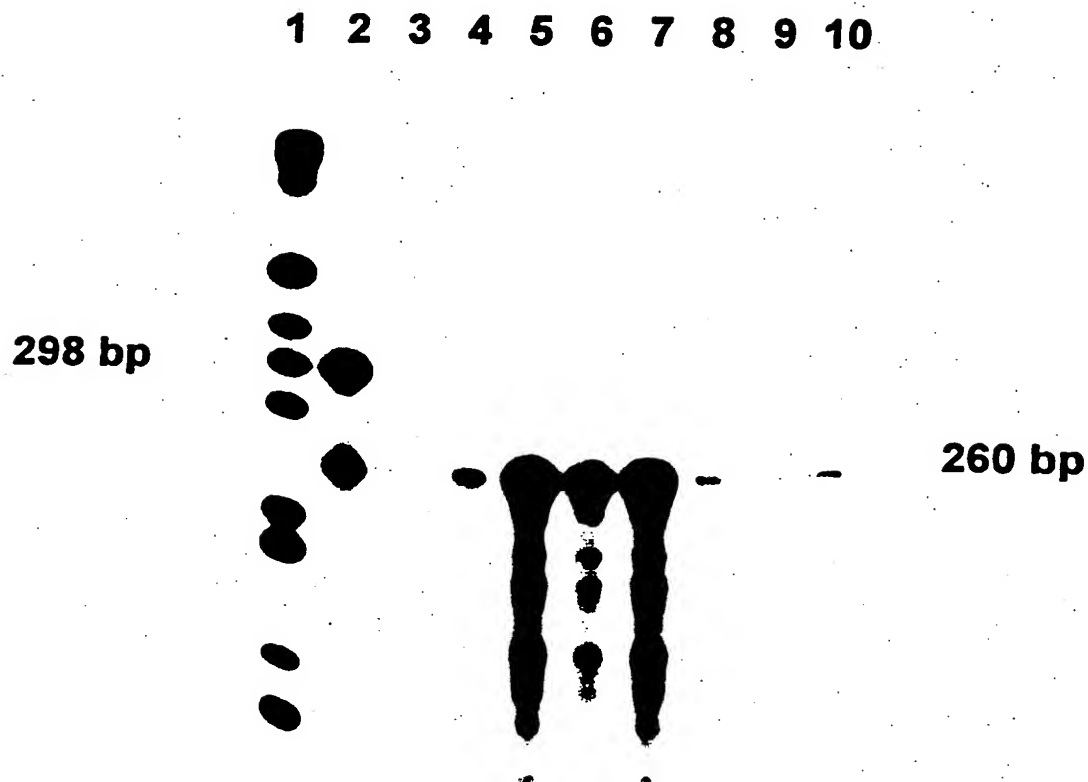
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

400

350

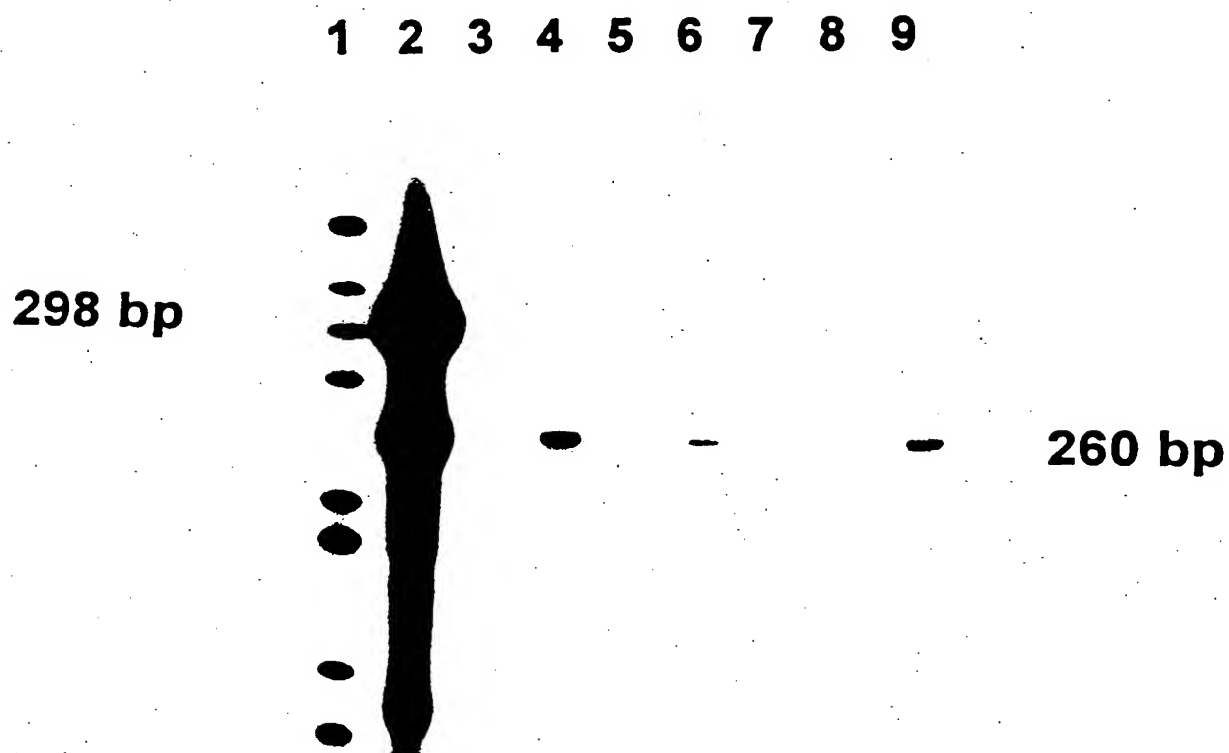
39/130

FIGURE 21



40/130

FIGURE 22



41/130
FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

42/130

FIGURE 24A

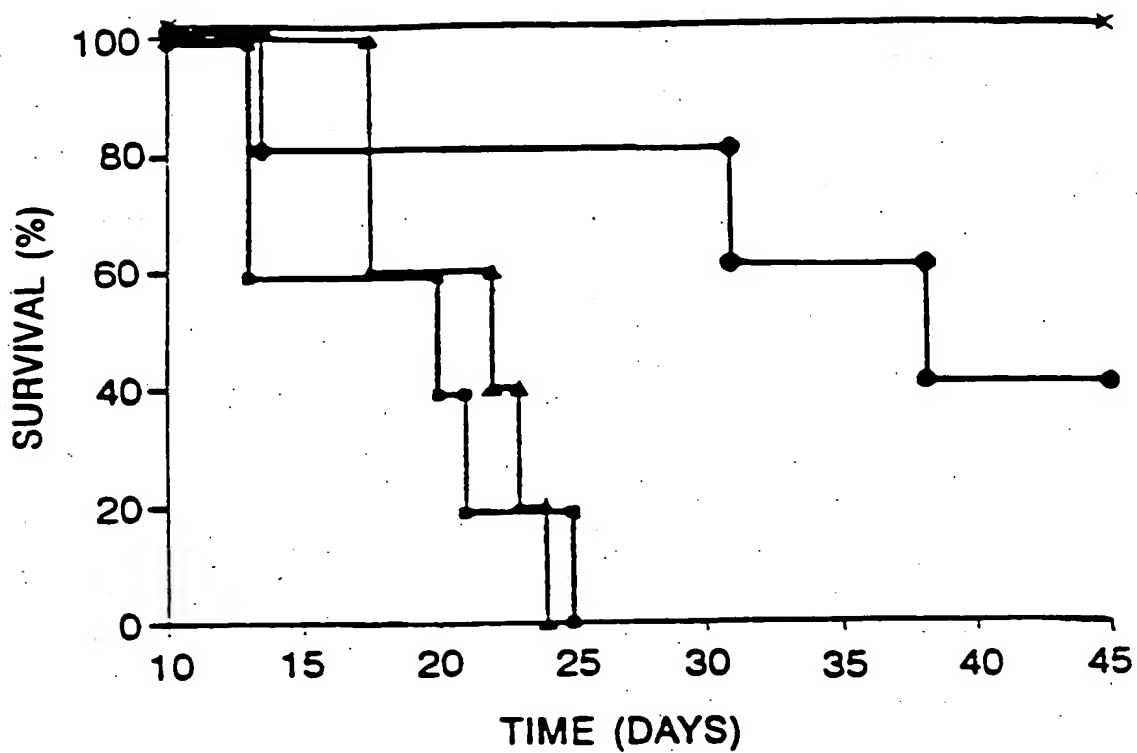
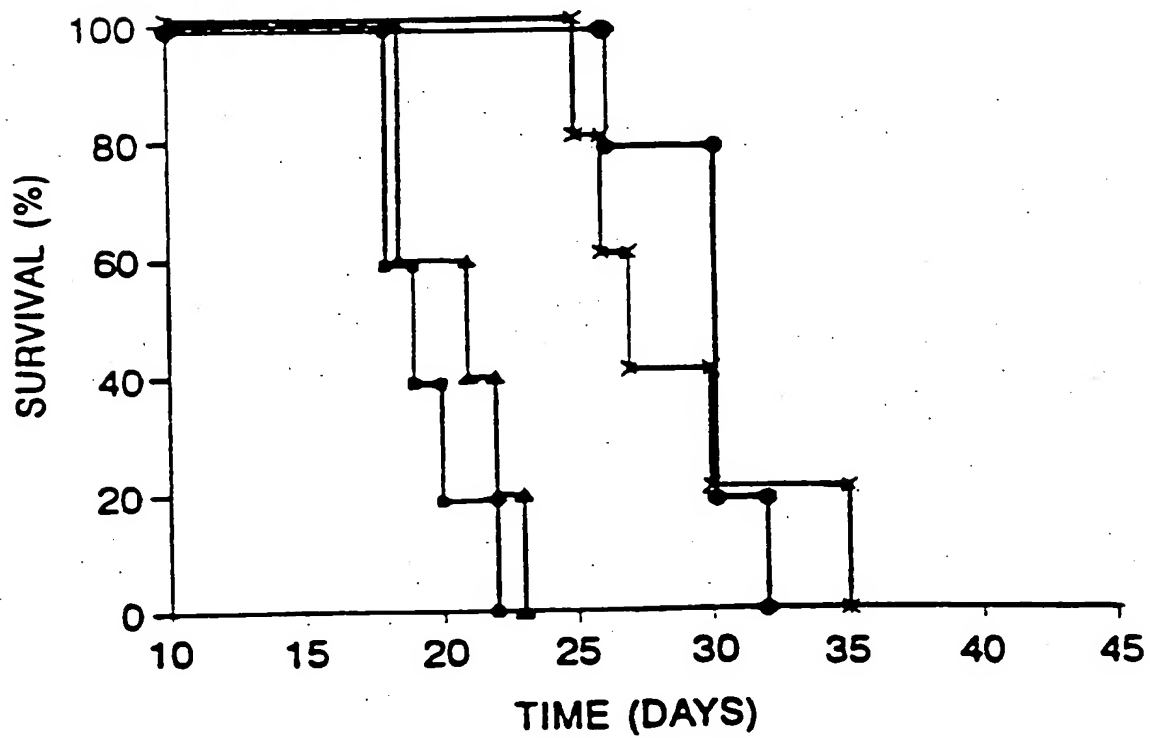


FIGURE 24B



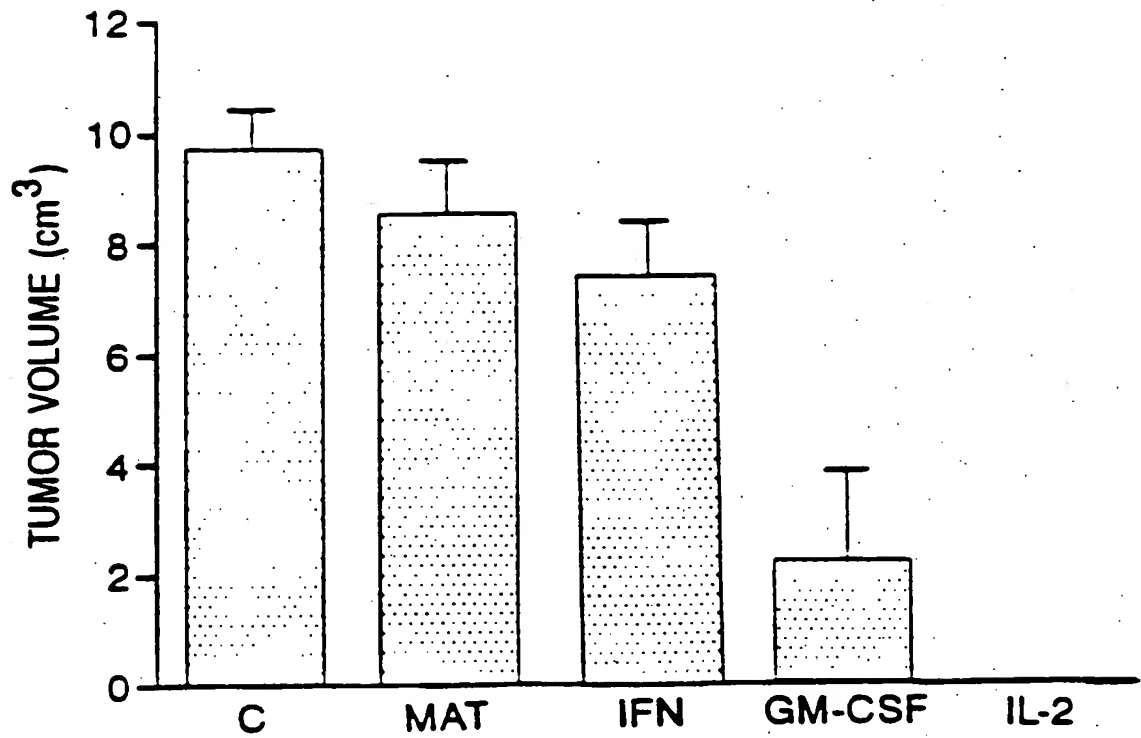
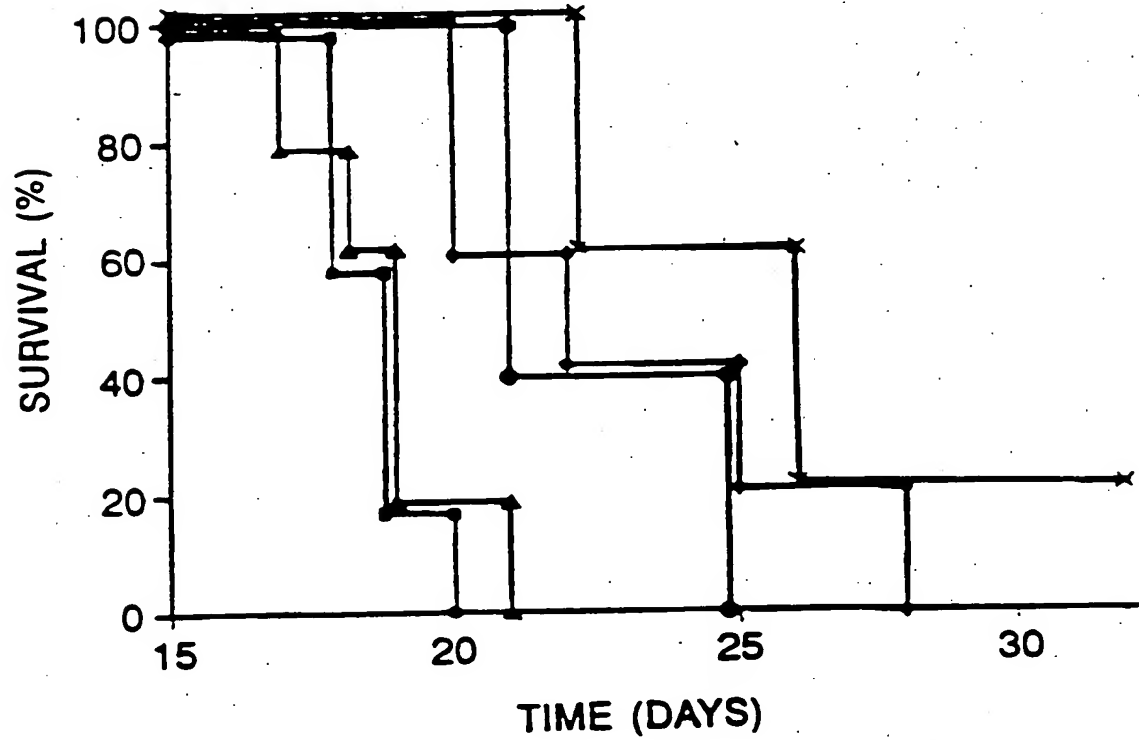
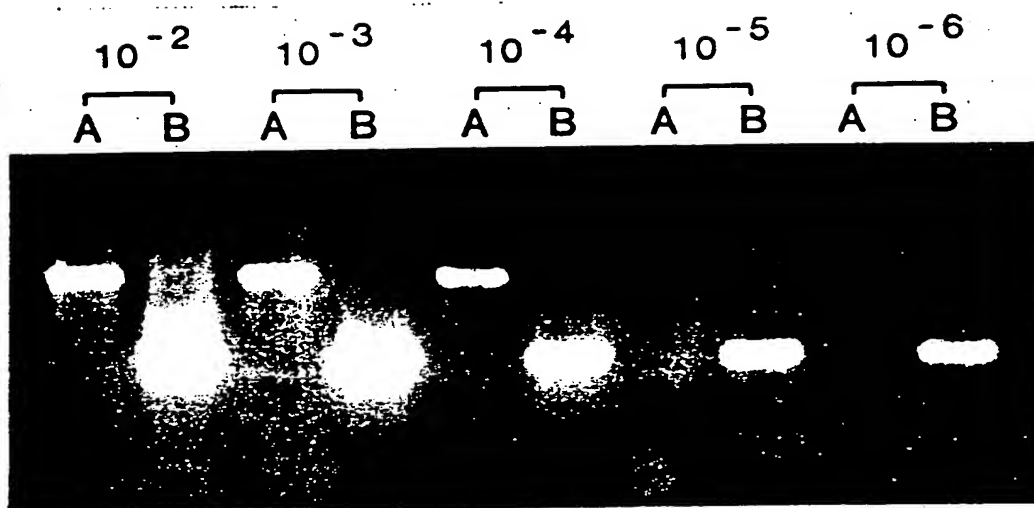
43/130
FIGURE 25A

FIGURE 25B



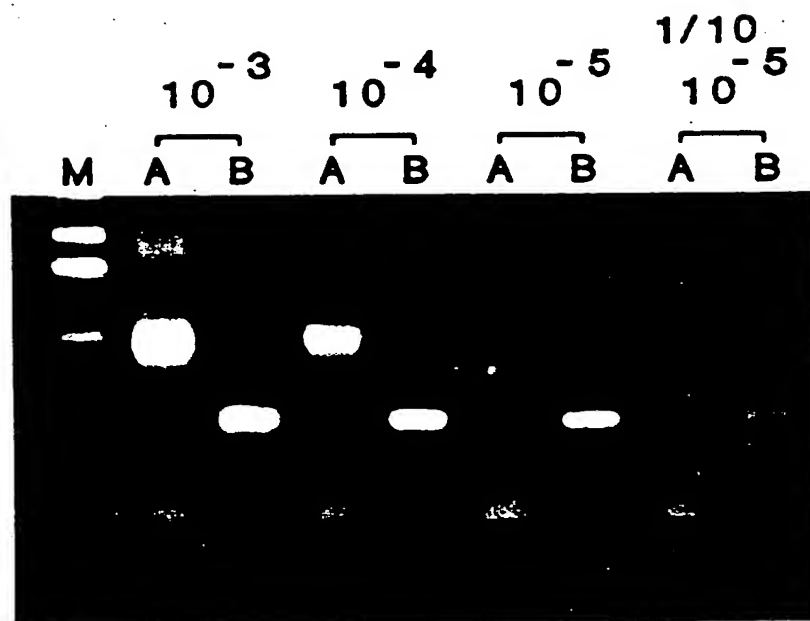
44/130

FIGURE 26



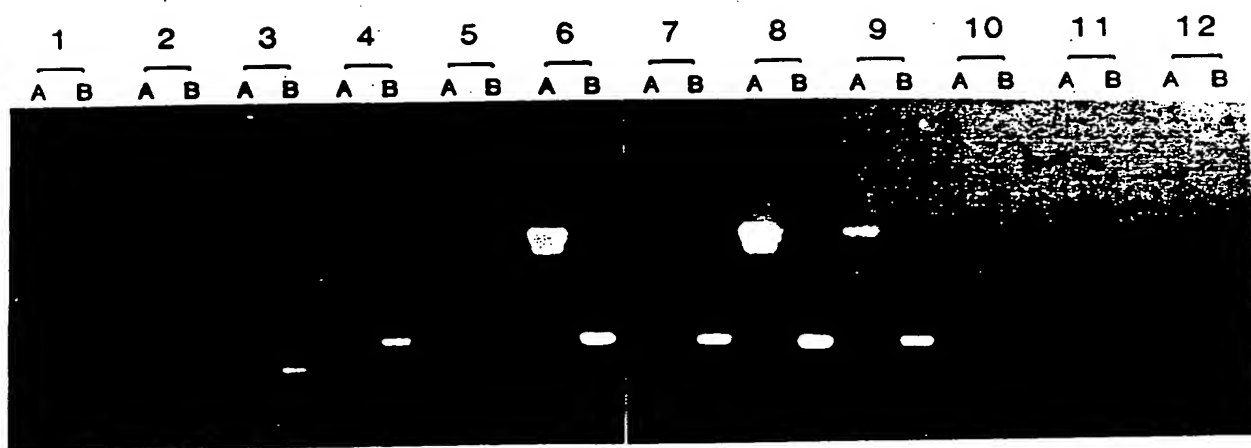
45/130

FIGURE 27



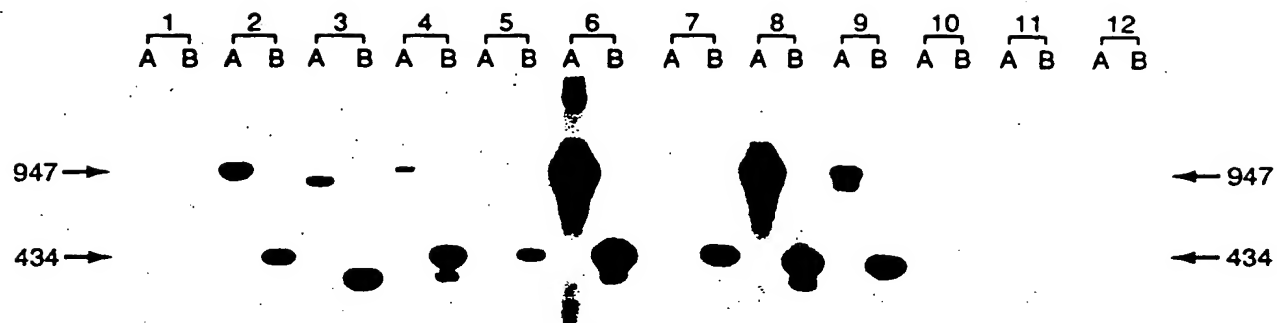
46/130

FIGURE 28



47/130

FIGURE 29



48/130

FIGURE 30

Patient	Stage	Tr atm nt	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	-	+
2	T2NoMo	RRP 7/93	6.1	-	-	+
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+
6	Recur T3	I-125 1986	54.7	1.4	-	+
7	T3ANoMo	RRP 10/92	NMA	0.3	-	+
8	T3NxMo	XRT 1987	7.5	0.1	-	-
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-
10	D2	S/P XRT Flutamide + Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	-	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	-	-
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-

49/130

FIGURE 31A

	10	20	30	40	50	60
1	AAGGGTGCTC TTCCCACGAG	CTTAGGCTGA GAATCCGACT	ATGCTTGCAG TACGAACGTC	ACAGGATGCT TGTCTACGA	TGGTTACAGA ACCAATGTCT	TGGGCTGTGA ACCCGACACT
61	CTCGAGTGGA GAGCTCACCT	GTTTTATAAG CAAAATATTC	GGTGCTCCTT CCACGAGGAA	AGGCTGAATG TCCGACTTAC	CTTGCAGACA GAACGTCTGT	GGATGCTTGG CCTACGAACC
121	TTACAGATGG AATGTCTACC	GCTGTGAGCT CGACACTCGA	GGGTGCTTGT CCCACGAACA	AAGAGGATGC TTCTCCTACG	TTGGGTGCTA AACCCACGAT	AGTGAGCCAT TCACTCGGTA
181	TTGCAGTTGA AACGTCAACT	CCCTATTCTT GGGATAAGAA	GGAACATTCA CCTTGTAAGT	TTCCCCTCTA AAGGGGAGAT	CCCCTGTTTT GGGGACAAAG	TGTTCTGCCC ACAAGGACGG
241	AGCTAAGCCC TCGATTTCGG	ATTTTTTCATT TAAAAAGTAA	TTTCTTTTAA AAAGAAAATT	CTCCTTAGCG GAGGAATCGC	CTCCGCAAAA GAGGCGTTTT	CTTAATCAAT GAATTAGTTA
301	TTCTTTAAAC AAGAAATTTG	CTCAGTTTTTC GAGTCAAAAG	TTATCTGTAA AATAGACATT	AAGGTAAATA TTCCATTTAT	ATAATACAGG TATTATGTCC	GTGCAACAGA CACGTTGTCT
361	AAAATCTAGT TTTTAGATCA	GTGGTTTACA CACCAAATGT	TAATCASCCTG ATTAGTGAGC	TTAGAGATTT AATCTCTAAA	TAAATTATTT ATTTAATAAA	CAGGATAAGT GTCCTATTCA
421	CATGATAATT GTACTATTAA	AAATGAAATA TTTACTTTAT	ATGCACATAA TACGTGTATT	AGCACATAGT TCGTGTATCA	GTGGTGTCCT CACCACAGGA	CCATATAGAA GGTATATCTT
481	AATGCTCAGT TTACGAGTCA	ATATTGGTTA TATAACCAAT	TTAACTACTT AATTGATGAA	GTTGAAGGTT CAACTTCCAA	TATCTTCTCC ATAGAAGAGG	ACTAAACTGT TGATTTGACA
541	AAGTTCCACA TTCAAGGTGT	AGCCTTACAA TCGGAATGTT	TATGTGACAG ATACACTGTC	ATATTCATTC TATAAGTAAG	ATTGTCTGAA TAACAGACTT	TTCTTCAAAT AAGAAGTTTA
601	ACATCCTCTT TGTAGGAGAA	CACCATAGCG GTGGTATCGC	TCTTATTAAT AGAATAATTA	TGAATTATTA ACTTAATAAT	ATTGAATAAA TAACTTATTT	TTCTATTGTT AAGATAACAA
661	CAAAAATCAC GTTTTTAGTG	TTTTATATTT AAAATATAAA	AACTGAAATT TTGACTTTAA	TGCTTACTTA ACGAATGAAT	TAATCACATC ATTAGTGTAG	TAACCTTCAA ATTGGAAGTT
721	AGAAAACACA TCTTTTGTGT	TTAACCCTT AATTGGTTGA	GTAAGGGGTA CATGACCCAT	ATGTTACTGG TACAATGACC	GTGATCCAC CACTAGGGTG	GTTTTACAAA CAAAATGTTT

50/130

FIGURE 31B

```

781 TGAGAAGATA TATTCTGGTA AGTTGAATAC TTAGCACCCA GGGGTAATCA GCTTGGACAG
    ACTCTTCTAT ATAAGACCAT TCAACTTATG AATCGTGGGT CCCCATTAGT CGAACCTGTC

841 GACCAGGTCC AAAGACTGTT AAGAGTCTTC TGA CTCCAAA CTCAGTGCTC CCTCCAGTGC
    CTGGTCCAGG TTTCTGACAA TTCTCAGAAG ACTGAGGTTT GAGTCACGAG GGAGGTCACG

901 CACAAGCAAA CTCCATAAAG GTATCCTGTG CTGAATAGAG ACTGTAGAGT GGTACAAAGT
    GTGTTCGTTT GAGGTATTTC CATAGGACAC GACTTATCTC TGACATCTCA CCATGTTTCA

961 AAGACAGACA TTATATTAAG TCTTAGCTTT GTGACTTCGA ATGACTTACC TAATCTAGCT
    TTCTGTCTGT AATATAATTC AGAATCGAAA CACTGAAGCT TACTGAATGG ATTAGATCGA

1021 AAATTTTCAGT TTTACCATGT GTAAATCAGG AAGAGTAATA GAACAAACCT TGAAGGGTCC
    TTTAAAGTCA AAATGGTACA CATTTAGTCC TTCTCATTAT CTTGTTTGGA ACTTCCCAGG

1081 CAATGGTGAT TAAATGAGGT GATGTACATA ACATGCATCA CTCATAATAA GTGCTCTTTA
    GTTACCACTA ATTTACTCCA CTACATGTAT TGTACGTAGT GAGTATTATT CACGAGAAAT

1141 AATATTAGTC ACTATTATTA GCCATCTCTG ATTAGATTTG ACAATAGGAA CATTAGGAAA
    TTATAATCAG TGATAATAAT CGGTAGAGAC TAATCTAAAC TGTTATCCTT GTAATCCTTT

1201 GATATAGTAC ATTCAGGATT TTGTTAGAAA GAGATGAAGA AATTCCCTTC CTTCTGCCC
    CTATATCATG TAAGTCCTAA AACAACTCTT CTCTACTTCT TTAAGGGAAG GAAGGACGGG

1261 TAGGTCATCT AGGAGTTGTC ATGGTTCATT GTTGACAAAT TAATTTTCCC AAATTTTTC
    ATCCASTAGA TCCTCAACAG TACCAAGTAA CAACTGTTTA ATTAAGGAGG TTTAAAAAGT

1321 CTTTGCTCAG AAAGTCTACA TCGAAGCACC CAAGACTGTA CAATCTAGTC CATCTTTTTC
    GAAACGAGTC TTTCAGATGT AGCTTCGTGG GTTCTGACAT GTTAGATCAG GTAGAAAAAG

1381 CACTTAACTC ATACTGTGCT CTCCCTTTCT CAAAGCAAAC TGTTTGCTAT TCCTTGAATA
    GTGAATTGAG TATGACACGA GAGGGAAAGA GTTTCGTTTG ACAAACGATA AGGAACTTAT

1441 CACTCTGAGT TTTCTGCCTT TGCCTACTCA GCTGGCCCAT GGCCCCTAAT GTTCTTCTC
    GTGAGACTCA AAAGACGGAA ACGGATGAGT CGACCGGGTA CCGGGGATTA CAAAGAAGAG

1501 ATCTCCACTG GGTCAAATCC TACCTGTACC TTATGGTTCT GTTAAAGCA GTGCTTCCAT
    TAGAGGTGAC CCAGTTTAGG ATGGACATGG AATACCAAGA CAATTTTCGT CACGAAGGTA

1561 AAAGTACTCC TAGCAAATGC ACGGCCTCTC TCACGGATTA TAAGAACACA GTTTATTTTA

```

51/130

FIGURE 31C

```

TTTCATGAGG ATCGTTTACG TGCCGGAGAG AGTGCCTAAT ATTCTTGTGT CAAATAAAAT

1621 TAAAGCATGT AGCTATTCTC TCCCTCGAAA TACGATTATT ATTATTAAGA ATTTATAGCA
      ATTTTCGTACA TCGATAAGAG AGGGAGCTTT ATGCTAATAA TAATAATTCT TAAATATCGT

1681 GGGATATAAT TTTGTATGAT GATTCTTCTG GTTAATCCAA CCAAGATTGA TTTTATATCT
      CCCTATATTA AAACATACTA CTAAGAAGAC CAATTAGGTT GGTTCCTAACT AAAATATAGA

1741 ATTACGTAAG ACAGTAGCCA GACATAGCCG GGATATGAAA ATAAAGTCTC TGCCTTCAAC
      TAATGCATTC TGTCAATCGGT CTGTATCGGC CCTATACTTT TATTTTCAGAG ACGGAAGTTG

1801 AAGTTCCAGT ATTCTTTTCT TTCCTCCCCT CCCCTCCCCT CCCTTCCCCT CCCCTTCCTT
      TTCAAGGTCA TAAGAAAAGA AAGGAGGGGA GGGGAGGGGA GGAAGGGGA GGGGAAGGAA

1861 CCCTTTCCCT TCCCTTCCTT TCTTTCTTGA GGGAGTCTCA CTCTGTCACC AGGCTCCAGT
      GGGAAAGGGA AGGGAAGGAA AGAAAGAAGT CCCTCAGAGT GAGACAGTGG TCCGAGGTCA

1921 GCAGTGGCGC TATCTTGGCT GACTGCAACC TCCGCCTCCC CGGTTCAAGC GATTCTCCTG
      CGTCACCGCG ATAGAACCGA CTGACGTTGG AGGCGGAGGG GCCAAGTTCC CTAAGAGGAC

1981 CCTCAGCCTC CTGASTAGCT GGGACTACAG GAGCCCGCCA CCACGCCCAG CTAATTTTTG
      GGAGTCGGAG GACTCATCGA CCCTGATGTC CTCGGGCGGT GGTGCGGGTC GATTAAAAAC

2041 TATTTTTTAGT AGAGATGGGG TTTCACCATG TTGGCCAGGA TGGTCTCGAT TTCTCGACTT
      ATAAAAATCA TCTCTACCCC AAAGTGGTAC AACCGGTCCT ACCAGAGCTA AAGAGCTGAA

2101 CGTGATCCGC CTGTCTGGGC CTCCCAAAGT GCTGGGATTA CAGGCGTGAG CCACCACGCC
      GCACTAGGCG GACAGACCCG GAGGGTTTCA CGACCCTAAT GTCCGCACTC GGTGGTGCGG

2161 CGGCTTTAAA AAATGGTTTT GTAATGTAAG TGGAGGATAA TACCCTACAT GTTTATTAAT
      CCCGAAATTT TTTACCAAAA CATTACATTC ACCTCCTATT ATGGGATGTA CAAATAATTA

2221 AACATAAATA TTCTTTAGGA AAAAGGGCGC GGTGGTGATT TACACTGATG ACAAGCATTC
      TTGTTATTAT AAGAAATCCT TTTTCCCGCG CCACCACTAA ATGTGACTAC TGTTTCGTAAG

2281 CCGACTATGG AAAAAAAGCG CAGCTTTTTT TGCTCTGCTT TTATTCAGTA GAGTATTGTA
      GGCTGATACC TTTTTTTCGC GTCGAAAAAG ACGAGACGAA AATAAGTCAT CTCATAACAT

2341 GAGATTGTAT AGAATTTTCAG AGTTGAATAA AAGTTCCTCA TAATTATAGG AGTGGAGAGA
      CTCTAACATA TCTTAAAGTC TCAACTTATT TTCAAGGAGT ATTAATATCC TCACCTCTCT

```


52/130

FIGURE 31D

2401 GGAGAGTCTC TTTCTTCCTT TCATTTTAT ATTTAAGCAA GAGCTGGACA TTTTCCAAGA
 CCTCTCAGAG AAAGAAGGAA AGTAAAAATA TAAATTCGTT CTCGACCTGT AAAAGGTTCT

2461 AAGTTTTTTT TTTTAAAGGC GCCTCTCAAA AGGGGCCGGA TTTCTTCTC CTGGAGGCAG
 TTCAAAAAAA AAAAATTCCG CGGAGAGTTT TCCCCGGCCT AAAGGAAGAG GACCTCCGTC

2521 ATGTTGCCTC TCTCTCTCGC TCGGATTGGT TCAGTGCACT CTAGAAACAC TGCTGTGGTG
 TACAACGGAG AGAGAGAGCG AGCCTAACCA AGTCACGTGA GATCTTTGTG ACGACACCAC

2581 GAGAAACTGG ACCCCAGGTC TGGAGCGAAT TCCAGCCTGC AGGGCTGATA AGCGAGGCAT
 CTCTTTGACC TGGGGTCCAG ACCTCGCTTA AGGTCGGACG TCCCGACTAT TCGCTCCGTA

2641 TAGTGAGATT GAGAGAGACT TTACCCCGCC GTGGTGGTTG GAGGGCGCGC AGTAGAGCAG
 ATCACTCTAA CTCTCTCTGA AATGGGGCGG CACCACCAAC CTCCCGCGCG TCATCTCGTC

2701 CAGCACAGGC GCGGGTCCCG GGAGGCCGGC TCTGCTCGCG CCGAGATGTG GAATCTCCTT
 GTCGTGTCCG CGCCCAGGGC CCTCCGGCCG AAGCGAGCGC GGCTCTACAC CTTAGAGGAA

2761 CACGAAACCG ACTCGGCTGT GGCCACCGCG CGCCGCCCGC GCTGGCTGTG CGCTGGGGCG
 GTGCTTTGGC TGAGCCGACA CCGGTGGCGC GCGGCGGGCG CGACCGACAC GCGACCCCGC

2821 CTGGTGCTGG CGGGTGGCTT CTTTCTCCTC GGCTTCCTCT TCGGTAGGGG GCGCCTCGC
 GACCACGACC GCCCACCGAA GAAAGAGGAG CCGAAGGAGA AGCCATCCCC CCGCGGAGCG

2881 GGAGCAAACC TCGGAGTCTT CCCCCTGGTG CCGCGGTGCT GGGACTCGCG GGTCAGCTGC
 CCTCGTTTGG AGCCTCAGAA GGGGCACCAC GCGGCCACGA CCCTGAGCGC CCAGTCGACG

2941 CGAGTGGGAT CCTGTTGCTG GTCTTCCCCA GGGGCGGCGA TTAGGGTCGG GGTAATGTGG
 GCTCACCTA GGACAACGAC CAGAAGGGGT CCCCCCGCT AATCCCAGCC CCATTACACC

3001 GGTGAGCACC CCTCGAG
 CCACTCGTGG GGAGCTC

53/130

FIGURE 32

Potential binding sites on the PSM promoter*

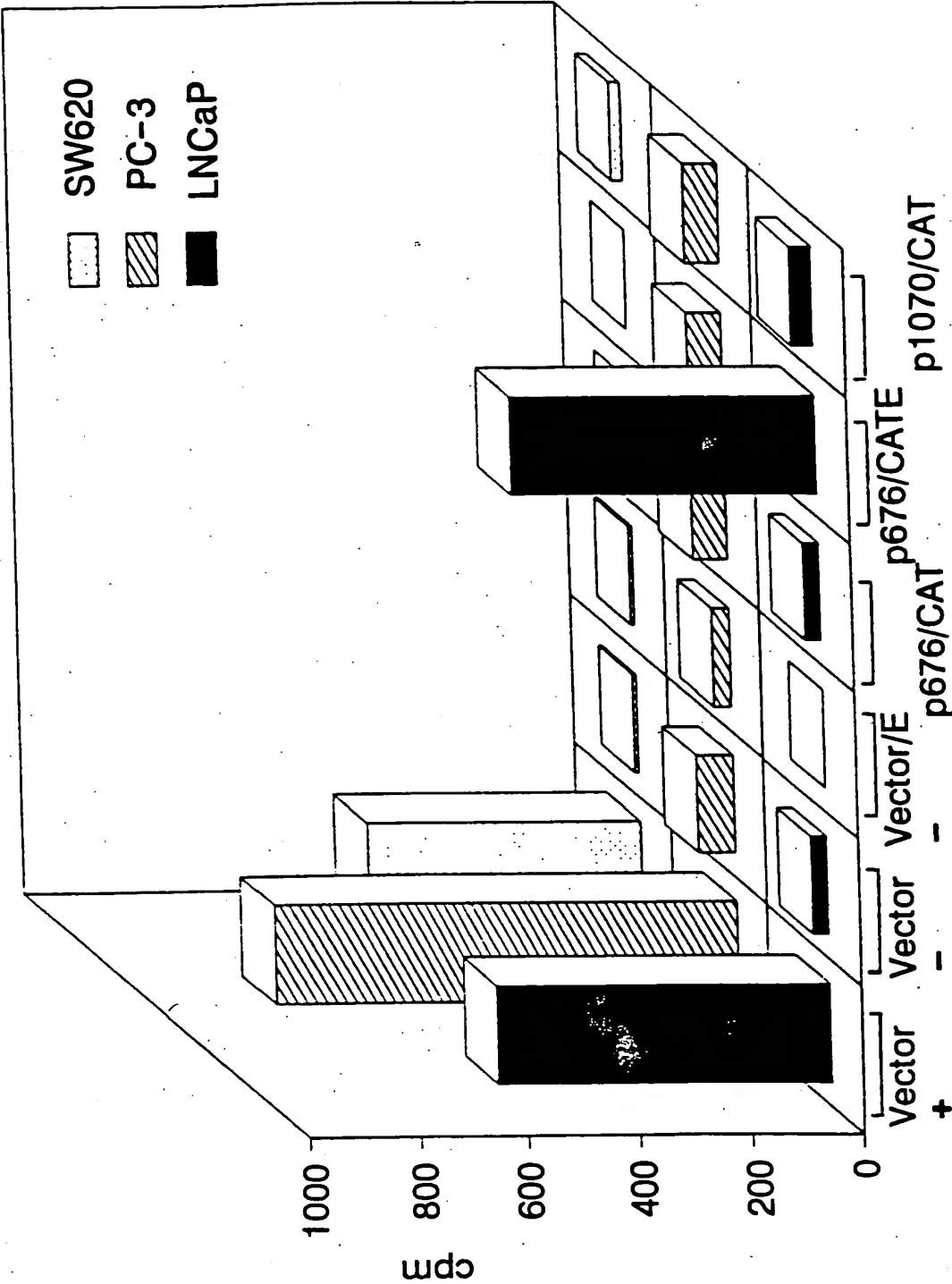
Site	Seq	**Location	#nt matched
AP1	TKAGTCA	1145	7/7
E2-RS	ACCN>NNNNNGGT	1940	12/12
		1951	12/12
GHF	NNNTAAATNNN	580	11/11
		753	11/11
		1340	11/11
		1882	11/11
		1930	11/11
		1979	11/11
		2001	11/11
		2334	11/11
		2374	11/11
		2591	11/11
		2620	11/11
		2686	11/11
JVC repeat	GGGNGGRR	1155	8/8
		1175	8/8
		1180	8/8
		1185	8/8
		1190	8/8
NFkB	GGGRHTYYHC	961	10/10
uteroglobi	RYYWSGTG	250	8/8
		921	8/8
		1104	8/8

IFN AAWAANGAAAGGR590 13/13 Cell 41:509 (1985)

* the PSM promoter sequence 683XFRVS (Fig. 1) starts from the 5' end of the promoter fragment. The 3' region overlaps the previously published PSM cDNA at nt#2485, i.e. the putative transcription start site is at nt#2485 on sequence 683XFRVS. **The number referred to in this table is in reference to sequence 683XF107 which is the complement and inverse of 683XFRVS.

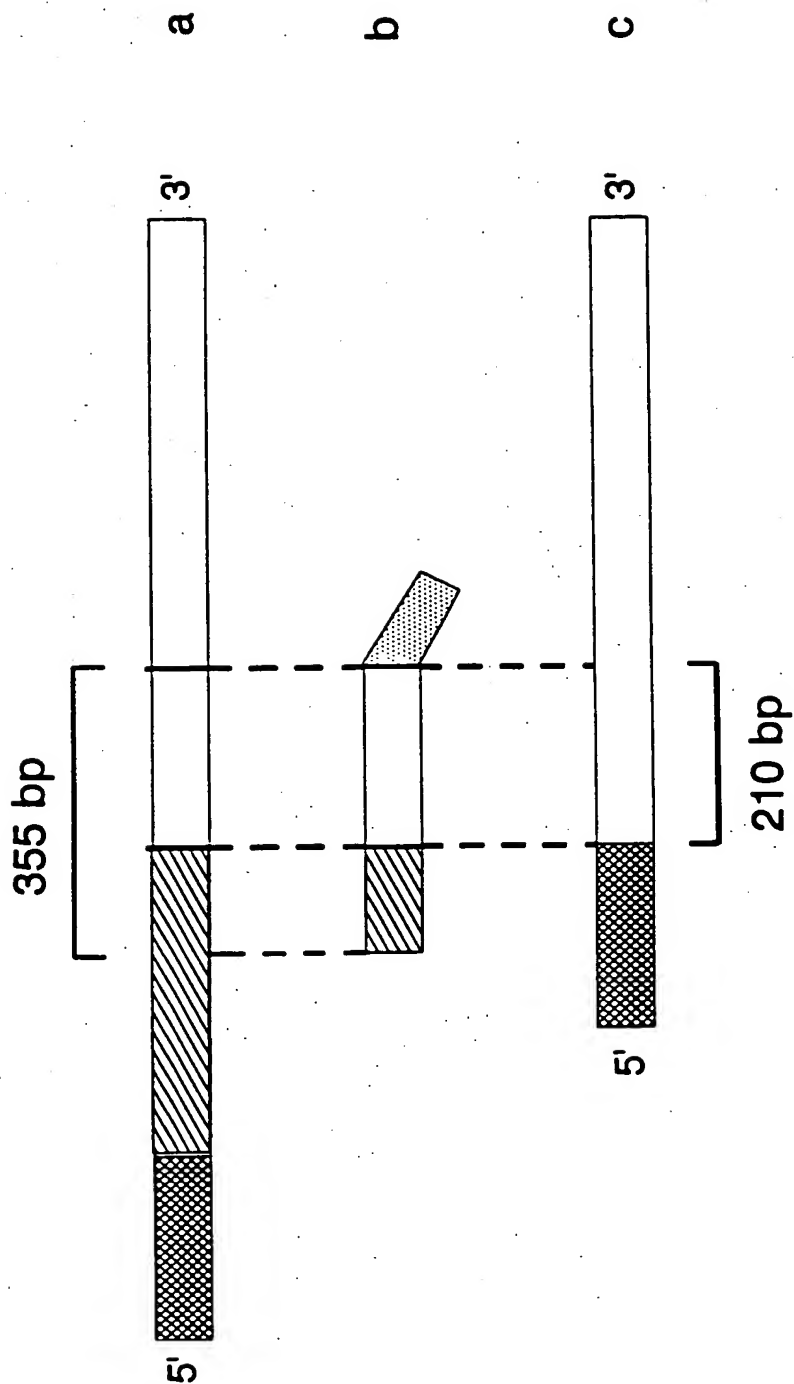
54/130

FIGURE 33



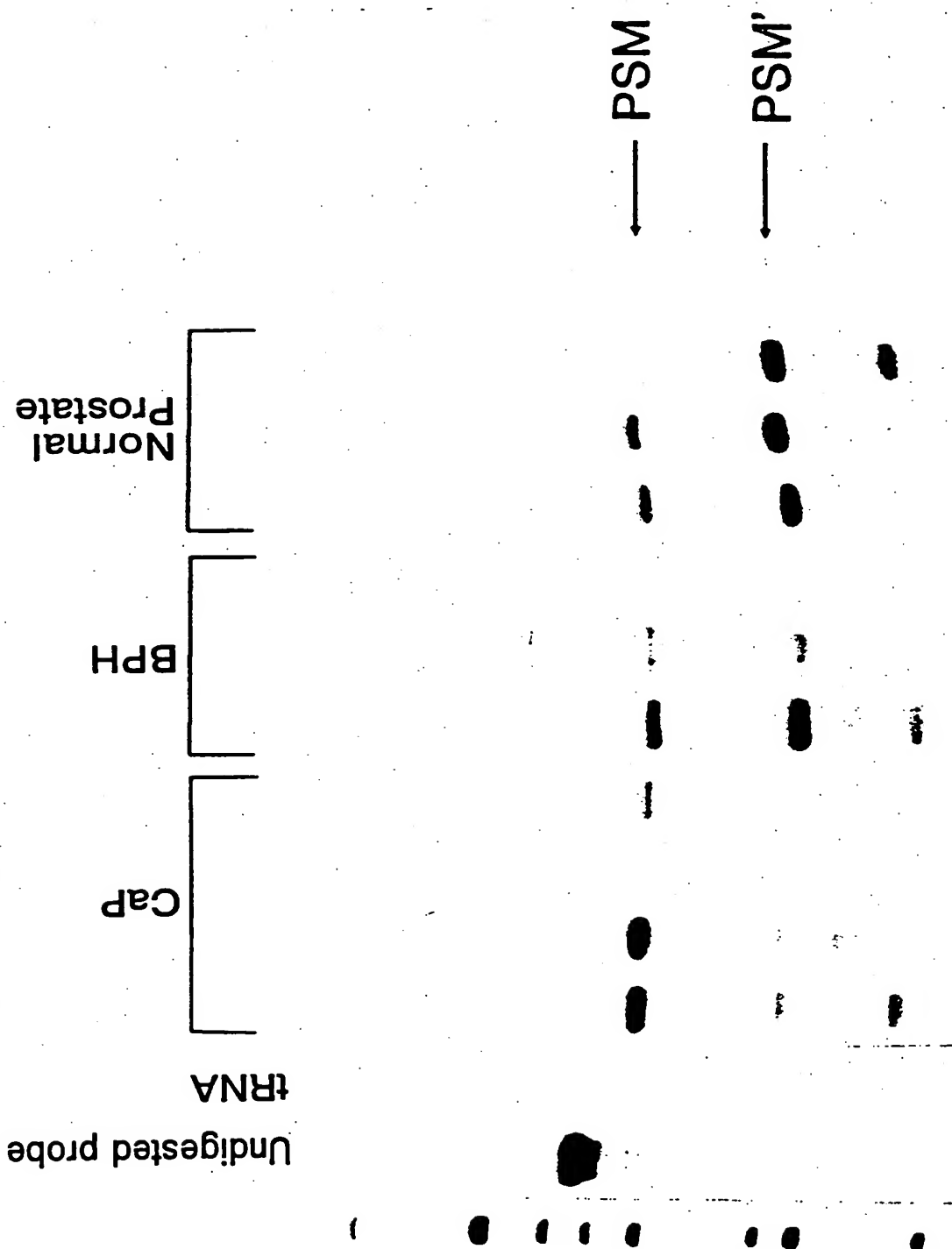
56/130

FIGURE 35



57/130

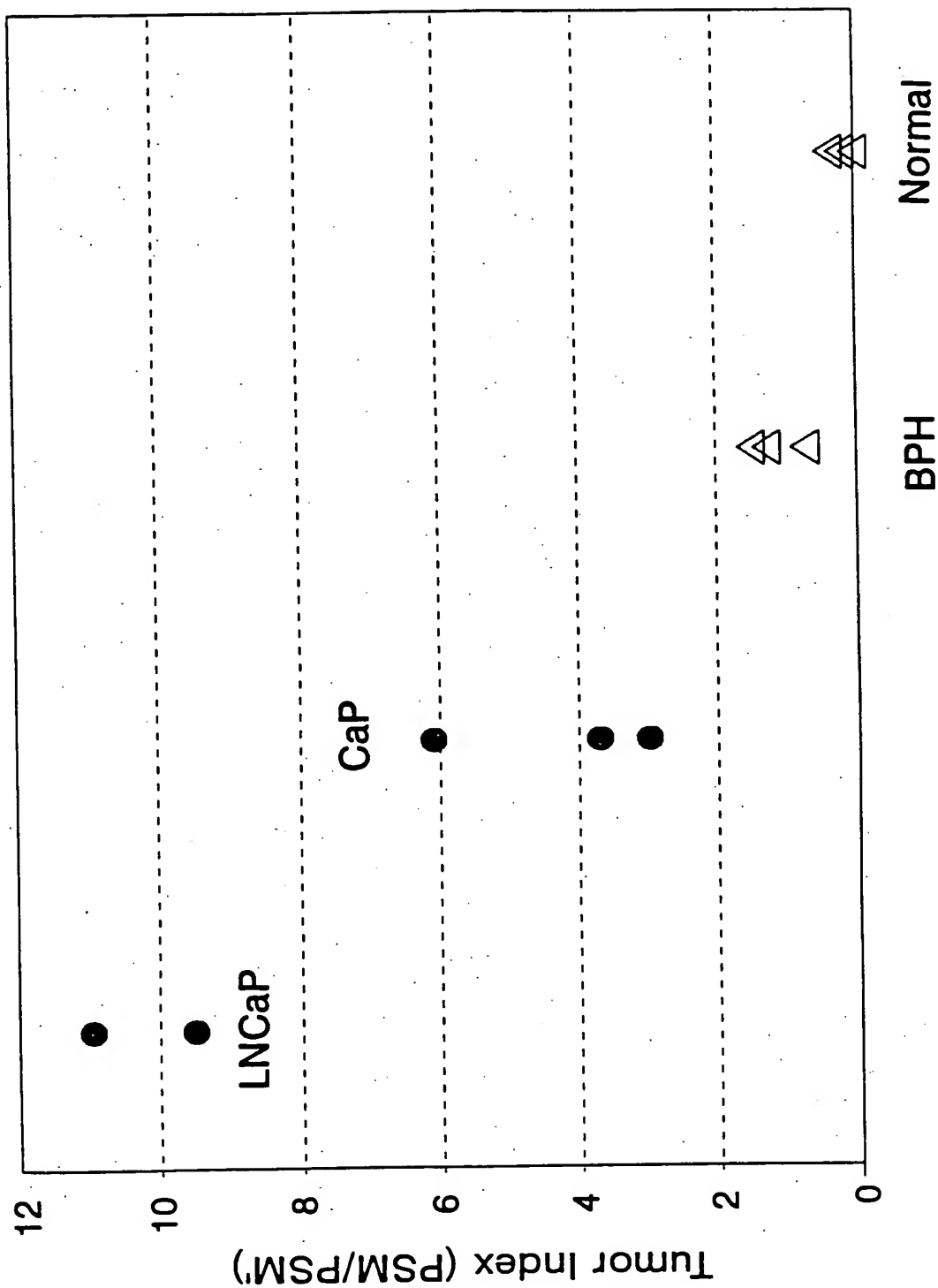
FIGURE 36



1 2 3 4 5 6 7 8 9 10 11 12

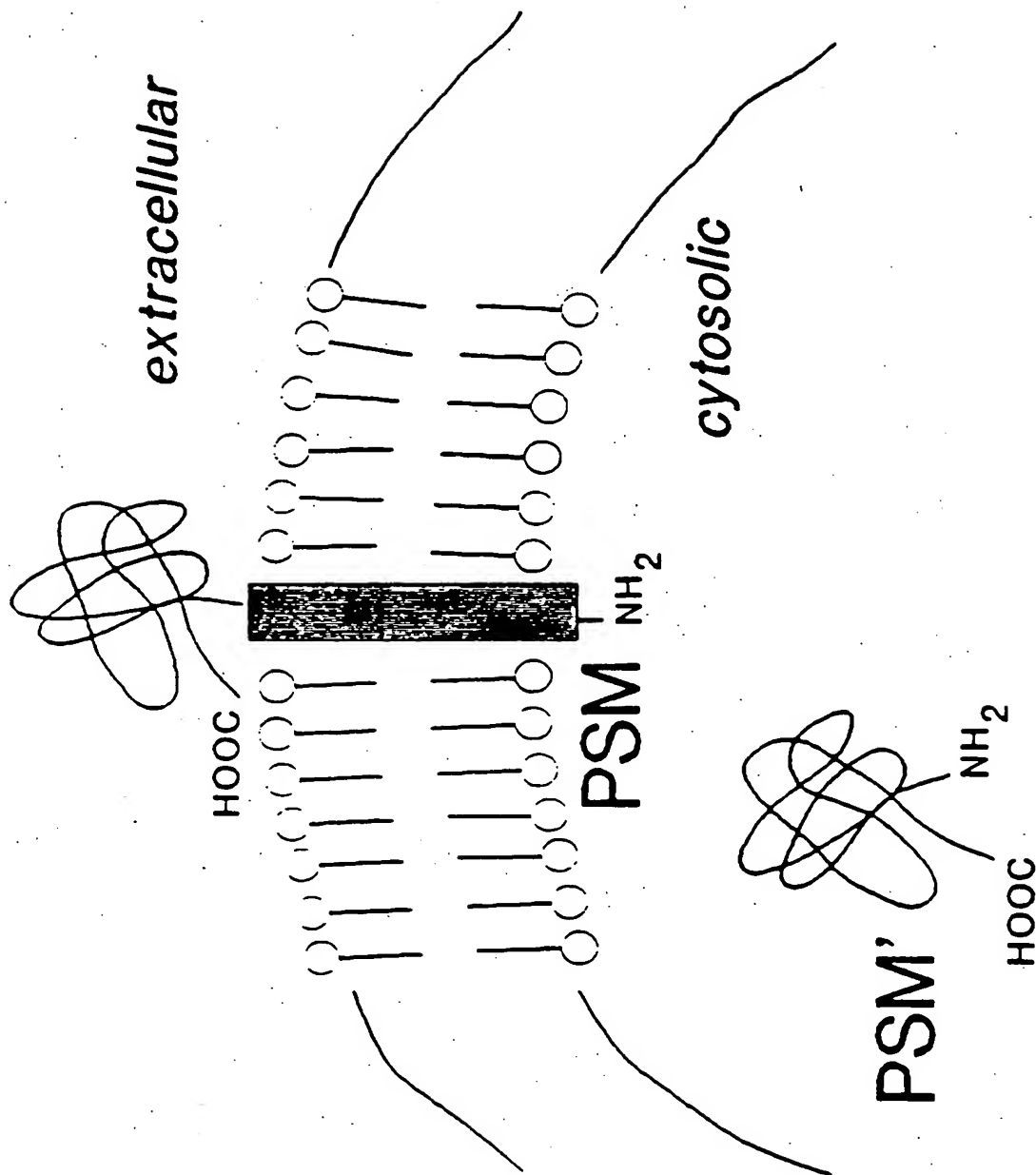
58/130

FIGURE 37



59/130

FIGURE 38



60/130

FIGURE 39

	10	20	30	40	50	60
1	TTTGCAGACT AAACGTCTGA	TGACCAACTT ACTGGTTGAA	TCTAAGAAAA AGATTCTTTT	GCAGAACCAC CGTCTTGGTG	ACAGGCAAGC TGTCCGTTTC	TCAGACTCTT AGTCTGASAA
61	TTATTAAATT AATAATTTAA	CCAGTTTTGA GGTCAAACT	CTTTGCCACT GAAACGGTGA	TCTTAGTGGC AGAATCACCG	CTTGAACAAG GAACTTGTTT	TTACCGAGTC AATGGCTCAG
121	CTCTCAGCGT GAGAGTCGCA	TAGTTACCCT ATCAATGGGA	ATTTTAATGA TAAAATTACT	TGAGGATAAT ACTCCTATTA	ATTATCTGCC TAATAGACGG	CAAATTATTG GTTTAATAAC
181	GSTATAGTAA CATATCATTT	TATATAGCAT ATATATCGTA	GTAAATCTCC CATTTAGAGG	TAGCAGAGTA ATCGTCTCAT	CTGGGATTTT GACCCTAAAG	GCCACTTTAT CGGTGAAATA
241	TTCTTCTTTA AAGAAGAAAT	CCAAGATACT GGTTCTATGA	CCTATTGGAC GSATAACCTG	TTAATACACA AATTATGTGT	GGACTAGTCT CCTGATCAGA	AAGGTATCAC TTCCATAGTG
301	CAGGTAGTCC GTCCATCAGG	ACTCCTGCTC TGAGGACGAG	GGAATCTGAC CCTTAGACTG	CCGGGATTAG GGCCCTAATC	AGTAGGGCAT TCATCCCCTA	GGACCAGATG CCTGGTCTAC
361	GGTTTAAACA CCAAATTTGT	AATTCAATAT TTAAGTTATA	CTTCCACTAG GAAGGTGATC	CTTCACCTTG GAAGTGGAAC	GGGTTGTAAA CCCAACATTT	AGTTTTTGAA TCAAAAACCT
421	CCACACACTG GGTGTGTGAC	TGCTCATAAC ACGAGTATTG	AATCTTCATC TTAGAAGTAG	TCTTAAAAGG AGAATTTTCC	ATTTTATTCT TAAAATAAGA	TCCTGGTATC AGGACCATAG
481	CTCACTCTCA GAGTGAGAGT	TCCCTTGAT AGGGAACATA	TCCGTGCTCA AGGCACGAGT	GTGGCTGACA CACCGACTGT	CAGAAGAGTT GTCTTCTCAA	CTTTATNNNN GAAATANNNN
541	NNNNNNNNNN NNNNNNNNNN	CATCCTGTTT GTAGGACAAG	ATTTTTTCAGA TAAAAAGTCT	TCTCAGTTCA AGAGTCAAGT	AGCATCTCGT TCGTAGAGCA	CCTCAGTGTG GGAGTCACAC
601	GTGTTNNCTG CACAAANGAC	ATCCCTCACT TAGGGAGTGA	CTAATCCAAG GATTAGGTTT	TCTTTCTGTT AGAAAGACAA	TTATGCACAG AATACGTGTC	GTTGGAATCT CAACCTTAGA
661	TATTTCCGTT ATAAAGGCAA	TGCGNNCCAA ACGCNNGGTT	TCNAATNGTA AGNTTANCAT	TTTAATATGC AAATTATACG	ATGTATATAT TACATATATA	GTATGTGCAT CATACACGTA
721	TTGTATGCTA AACATACGAT	NGCGATTAAG NCGCTAATTC	AACTAGAATA TTGATCTTAT	ATTAATAATT TAATTATTAA	GGAAGTCTAG CCTTCAGATC	AAGTGG TTCACC

61/130

FIGURE 40A

	10	20	30	40	50	60
1	TGAAAAATAC ACTTTTTATG	ATCAAAAATA TAGTTTTTAT	GGCATGAGAT CCGTA CTCTA	ACGAGCCTAT TGCTCGGATA	AGATAGGACT TCTATCCTGA	TATTTTTTAT ATAAAAAATA
61	TATTGTTGTA ATAACAACAT	TGTATTATTT ACATAATAAA	GTAAACACA CATTTTGTGT	AATTATCAAT TTAATAGTTA	ATTACCTCTG TAATGGAGAC	ACATTAGGTG TGTAATCCAC
121	AGATATTCTG TCTATAAGAC	AATTTTAATT TTAAAATTAA	TCTCTTGCCT AGAGAACGGA	ACTTTCAGTG TGAAAGTGAC	AAAAAGAGTC TTTTTCTCAG	ATGCAAAACA TACGTTTGTC
181	ATTTTAAAGT TAAAAATTCA	TGCAAACCAA ACGTTTG GTT	TTGCAAAATA AACGTTT TAT	TTTTTTTATC AAAAAAATAG	CAACTTCAAT GTTGAAGTTA	GATAGGTATT CTATCCATAA
241	GCTGTTAATT CGACAATTAA	CTAAGATATG GATTCTATAC	CATTAATTGT GTAATTAACA	TTCAACTAAT AAGTTGATTA	GGGTGTCAAA CCCACAGTTT	CGAGATGTTT GCTCTACAAG
301	TGAAAATGAA ACTTTTACTT	GGCAAAAAGG CCGTTTTTCC	AGATCCACCT TCTAGGTGGA	TCTACTTTCA AGATGAAAGT	TAAAGTTTCT ATTTCAAAGA	ATCTTCCTCT TAGAAGGAGA
361	GCTGACTCAA CGACTGAGTT	ATAAGCATTT TATTCSTAAA	AATACATTTT TTATGTAAAA	ATAACGAATT TATTGCTTAA	AATTATGAAT TTAATACTTA	ATATTTCAAA TATAAAGTTT
421	TAAATAAATT ATTTATTTAA	ATTTCCAAGT TAAAGGTTCA	GTTGAAGGAA CAACTTCCTT	ATTCAGACTT TAAGTCTGAA	CTAATTTGCT GATTAAACGA	CTGATTCTGA GACTAAGACT
481	AACTAAAACA TTGATTTTGT	AATGCTCTGT TTACGAGACA	GAGAGTTTGC CTCTCAAACG	GTTTCCAGTG CAAAGGTCAC	AATAGCGGTG TTCATCGCAC	AGAAATCCAA TCTTTAGGTT
541	GTCAGACAGC CAGTCTGTCTG	TACATGAAAC ATGTACTTTG	TACATTTACC ATGTAAATGG	AGCTCTCTGC TCGAGAGACG	CAGACACCAG GTCTGTGGTC	TGCACGATAG ACGTGCTATC
601	CGCAGAACAT GCGTCTTGTA	GTAGCTAGAT CATCGATCTA	CTCAGTCATA GAGTCAGTAT	GCTNNNNNNN CGANNNNNNN	NNNNNNNNNN NNNNNNNNNN	AGACCTTGCA TCTGGAACGT
661	GTTGGCTTTT CAACCGAAAA	AACCTGAAGG TTGGACTTCC	AGATAAGGCA TCTATTCCGT	AGATTCCAGG TCTAAGGTCC	GTTTATTTAG CAAATAAATC	AGAAATTACA TCTTTAATGT
721	GGATCTGGGA CCTAGACCCT	ATAAAGTAGT TATTTTCATCA	TACAAAATTA ATGTTTTAAT	GTCCCCAACC CAGGGGTTGG	AGCTTTCATG TCGAAAGTAC	GAGCTTTCAA CTCGAAAGTT

62/130

FIGURE 40B

781 TTATTAATTA TTCTAGTTCT TAATCGCATG CATACAATGC ACATACATAT ATACATGCAT
AATAATTAAT AAGATCAAGA ATTAGCGTAC GTATGTTACG TGTATGTATA TATGTACGTA

841 ATTAAAATAC ATGATTGGAC GCAAACGGAA ATAAGATTCC ACCTGTGCAT AAAACAGAA
TAATTTTATG TACTAACCTG CGTTTGCCTT TATTCTAAGG TGGACACGTA TTTTGTCTTT

901 GACTTGGTTA GAGTGAGGGA TCAGGAAACA CCACACTGAG GACGAGATGN NNNNNNNNNN
CTGAACCAAT CTCACCTCCCT AGTCCTTTGT GGTGTGACTC CTGCTCTACN NNNNNNNNNN

961 NTAGTGGGTG GGGGGCGGAC ATCAATAAAG AACTCTTCTG TGTGAGCCAC TGAGCACGGA
NATCACCCAC CCGCCGCGCTG TAGTTATTTT TGTAGAAGAC ACASTCGGTG ACTCGTGCCT

1021 ATAAAGGGAT GAGASTGAGG GCAANTACCA GAAGAATAAA ATCCTTTTAA GAGATGAAGA
TATTTCCCTA CTCTCACTCC CGTTNATGGT CTTCTTATTT TAGGAAAATT CTCTACTTCT

1081 TTGTTATGAG CACAGTGTGT GGNTTCAAAA ATCTTTTAAC AACCCCAAGG TGAAGCTAGT
AACAATACTC GTGTACACACA CCNAAGTTTT TAGAAAATTG TTGGGGTTCC ACTTCGATCA

1141 TGGAAGATAT TTGAATTTGT TTAAACCCAT CTGGTCCTAG CCCTATTCTT TGAATCCGAA
ACCTTCTATA AACTTAAACA AATTTGGGTA GACCAGGATC GGGATAAGAA ACTTAGGCTT

1201 GAGGTCAAGA ATTCCGAGCA GASTGSACTA CCTGTGATAC CTTAGACTAG TCCTGTGTAT
CTCCAGTTCT TAAGGCTCGT CTCACCTGAT GGACACTATG GAATCTGATC AGGACACATA

1261 TCAAGTCCAA TGAGAGTATC TGTAAGAGAA TAAGTGCGAA ATCCAGATCT
AGTTCAGGTT ACTCTCATAG ACATTCTCTT ATTCACGCTT TAGGTCTAGA

63/130

FIGURE 41

	10	20	30	40	50	60
1	GGATTCTGTT CCTAAGACAA	GAGCCCTAGC CTCGGGATCG	TCATTATGAT AGTAATACTA	GTCCTGTTGT CAGGACAACA	CCTACCCAAA GGATGGGTTT	TAAGACTCAT ATTCTGAGTA
61	CCCAACTACA GGGTTGATGT	TCTCAATAAT AGAGTTATTA	TAATGAAGAT ATTACTTCTA	GGAAATGAGG CCTTTACTCC	TAAAAAATAA ATTTTATTAT	ATAAATAAAT TATTTATTTA
121	AAAAGAAACA TTTTCCTTGT	TTCCCCCCCC AAGGGGGGGT	TTTATTATTT AAATAATAAA	TTTCAAATAC AAAGTTTATG	CTTCTATGAA GAAGATACTT	ATAATGTTCT TATTACAAGA
181	ATCCCTCTCT TAGGGAGAGA	AAATATTAAT TTTATAATTA	AGAAATCAAT TCTTTAGTTA	ATTATTGGAA TAATAACCTT	CTGTGAATAC GACACTTATG	CTTTAATATC GAAATTATAG
241	TCATTATCCG ASTAATAGGC	GTGTCAACTA CACAGTTGAT	CTTTCCTATG GAAAGGATAC	ATGTTGAGTT TACAACTCAA	ACTGGGTTTA TGACCCAAAT	GAAGTCGGGA CTTCAGCCCT
301	AATAATGCTG TTATTACGAC	TAAANNNNNN ATTTNNNNNN	AGTTAGTCTA TCAATCAGAT	CACACCAATA GTGTGGTTAT	TCAAATATGA AGTTTATACT	TATACTTGTA ATATGAACAT
361	AACCTCCAAG TTGGAGGTTG	CATAAAAAGA GTATTTTCTT	GATACTTTAT CTATGAAATA	AAAAGAGGTT TTTTCTCCAA	CTTTTTTTCT GAAAAAAGA	TTTTTTTTTT AAAAAAAAAA
421	TCCAGATGGA AGGTCTACCT	GTTCCTCTCC CAAATGAGG	TGTCAGGCAG ACAGTCCGTC	GCNGAGTGCA CGNCTCACGT	GTGGTGCCAT CACCACGGTA	CTCGGCTCAC GAGCCGAGTG
481	TGCAACCTCC ACGTTGGAGG	ACCTCCCATG TGGAGGGTAC	TTTAAAGGAT AAGTTCCCTA	TCTCCTTCCT AGAGGAAGGA	CAGTCTCCTG GTCAGAGGAC	AGTAGCTGGG TCATCGACCC
541	ATTACAGGTG TAATGTCCAC	TGCACCACCA ACGTGGTGGT	CACCCAGCTA GTGGGTGAT	ATTTTGTAT TAAAAACATA	TTTTAATAGA AAAATTATCT	GACAGGGTTT CTGTCCCAA
601	CGATCGATGT GCTAGCTACA	TGGCCAGGCT ACCGGTCCGA	AGTCTCGAAC TCAGAGCTTG	TCCTGACCTC AGGACTGGAG	TAGGTGATCC ATCCACTAGG	ACCCGCTCAG TGGGCGAGTC
661	CTCCCAAAGT GAGGGTTTCA	TGTAGAATTA ACATCTTAAT	CACGTGTGAG GTGCACACTC	GCACTGCGCC CGTGACGCGG	TTGCCAGGAG AACGGTCCTC	ATACATTTT TATGTAAAAA
721	GATAGGTTTA CTATCCAAAT	ATTTATAAAG TAAATATTTT	CACTGCACA TGTGACGTGT	GATTTGAGTT CTAAACTCAA	GCTGGGAAAT CGACCTTTTA	GCACGGATTC CGTGCCTAAG
781	CAGTATGCA GTCATACGT					

64/130

FIGURE 42

10 20 30 40 50 60
1 AATCAAAATA AAACAGTTAA AGTTTCAATTA CTATTAATCAA ACACAAAATA AATGAATATTT
TTAGTTTAT TTGTCAATTT TCAAACTAAT GATAATAGTT TGTGTTTT TTACITATAA
61 ATCTTTTATG TCAGTAGAGG GTCAATTAAT CCTTCAAGGAT TTGTATGATA GTATCAGATA
TAGAAAATAC AGTCATCTCC CAATTAATTA GGAAATCCTA AAACACTACTAT CATAGTCTAT
121 CCCAGCACTA TGCATAGAAGT TTGTGAAGAAT TCACGAGATG AATAAATCAC AGATTCTGTC
GGTTCGTGAT ACCATCTTCA ACATCTCTTA AGTGCCTAC TTATTTTAGTG TCTAAGACAG
181 CTCAAAATGG TTAGATCTAT TCAGGAACA AAGCTAATAA AACCCACCA ATAACTAAAA
GAGTTTACC AATCTAGATA AGTCCTTTCT TTCCGATTTT TTGGGGTGGT TATTGATTTT
241 ATCAACCAA TGAAAAACAA CAATCATAA ATAAGTAAGT ACCATAGAA AGAAAAGCTC
TAGTTGGTTT ACTTTTGT GTTAGTATTT TATTCATTTCA TGGATATCTT TCTTTTCGAG
301 AGAGGAGGTA AAAGAATCT CCTTAAAGG AATACATAT ACTGTAAAC TGTGACTGAT
TCTCCTCCAT TTTTCTTAGA GGAATTTTCC TTATGATATA TGACATTTTG AACTGACTA
361 AGAAGGAA
TCTTCCTT

65/130

FIGURE 43A

	10	20	30	40	50	60
1	TATGGGAAAG ATACCCTTTC	TTTTCAGAGG AAAAGTCTCC	AAATAAGGTA TTTATTCAT	AGGGAAAAGT TCCCTTTTCA	TATCTCTTTT ATAGAGAAAA	TTTCTCTCCC AAAGAGAGGG
61	CCAATGTAAA GGTTACATTT	AAGTTATAGT TTCAATATCA	GGGTTTTACA CCCAAAATGT	TGTGTAGAAT ACACATCTTA	CATTTTCTTA GTAAAAGAAT	AAACTTTATG TTTGAAATAC
121	AATACCATTA TTATGGTAAT	TTTTCTTGTA AAAAGAACAT	TTCTGTGACA AAGACACTGT	TGCCACCTTA ACGGTGGAAT	CAGAGAGGAC GTCTCTCCTG	ACATTTACTA TGTAATATGAT
181	GGTTATATCC CCAATATAGG	CGGGGTTAAA GCCCCAATTT	TTGAGCATT AAGCTCGTAA	GGAATTTGGC CCTTAAACCG	CAGTGTAGAT GTCACATCTA	GTTTAGAGTG CAAATCTCAC
241	AACAGAACAA TTGTCTTGT	TTTTTCTGTG AAAAAGACAC	CTTACAGGTT GAATGTCCAA	ATGGCTGTGG TACCGACACC	CGTACAAAGAA GCATGTTCTT	GCATGCACTG CGTACGTGAC
301	GGTTTATTAT CCAAATAATA	TAACTTTCAG ATTGAAAGTC	TATCTTTGTT ATAGAAACAA	TTAAATATT AATTTATAAA	TCTACAAAAA AGATGTTTTT	TGTTTACTAA ACAAATGATT
361	ATTAAATTGT TAATTTAACA	AGTATGAATT TCATACTTAA	GTTATAAATA CAATATTTAT	ATGAGGAAAA TACTCCCTTT	CATTTACACA GTAAATGTGT	TAGCAAATTT ATCGTTTAAA
421	AAAAATTACT TTTTTAATGA	GTCAATTTGAT CAGTAAACTA	TTGTTAATAT AATTAATTATA	ATTTTCTCT TAAAAAGAGA	TTAGTGGGAA AATCACCCTT	ATTAAATTAA TAATTTAATT
481	AAAATTCCTT TTTTAAGGAA	TGCACTGTCA AGCTGACAGT	GACAATAGGA CTGTTATCC	TTGCTGTGGT AACGACACCA	CTACTTGCTT GATGAACGAA	ATTATATTTG TAATATAAAC
541	TAGAGTCTAG ATCTCAGATC	AATGCAATCT TTACGTTASA	CACTACACTA GTGATGTGAT	TAGACATCTC ATCTGTAGAG	ANNCTAACGT TNNGATTGCA	AGGACAATTC TCCTGTTAAG
601	TGAGAAACTA ACTCTTTGAT	TTCCAGACCT AAGGTCTGGA	CGTTATGGGC GGAATACCCG	TTAGCCAAGG AATCGGTTCC	NTATCCTTCA NATAGGAAGT	GCTGGCATTG CGACCGTAAC
661	CAGGGTGAAT GTCCCACTGA	TCTNCCTCNV AGANGGAGNN	AATCCAGCTC TTAGGTCGAG	TCTNTCACAG AGANAGTGTC	ATGTGATCCA TACACTAGGT	AGAGACACTC TCTCTGTGAG
721	ACAATTAATC TGTTAATTAG	AACTAGCATT TTGATCGTAA	CTAAATTTCA GATTTAAAGT	ATTCCAGATC TAAGGTCTAG	TATTACCTTA ATAATGGAAT	ATATGGTAGC TATACCATCG

66/130

FIGURE 43B

781 TGAAGCTTTN NTCAGTGTCA ATTCTGATCA GATATATGAC AATTTTAAAT TATTTGCAGT
ACTTCGAAAN NAGTGACAGT TAAGACTAGT CTATATACTG TTAAAATTTA ATAAACGICA

841 GTGTAAGAAA CGCTTCAGGT AGTTTAAATT TAAGGCT
CACATTCTTT GCSAAGTCCA TCAAATTTAA ATTCCGA

67/130

FIGURE 44A

	10	20	30	40	50	60
1	CTCCTTTGGC GAGGAAACCG	CCCTGCCAGC GGGACGGTCG	TGGGCATTTT ACCCGTAAAA	TAACCTAGTT ATTGGATCAA	TACACAGTGT ATGTGTCACA	CTTTTTTTTCC GAAAAAAAGG
61	TTATTTTAAA AATAAAATTT	TTGTTTGTTC AACCAACAAG	CAGATTTCGGT GTCTAAGCCA	AATATCAATT TTATAGTTAA	TTTAATATTA AAATTATAAT	CACTTAAATG GTGAATTTAC
121	AGTACCAGAA TCAATGGTCTT	CTTTATCTTC GAAATAGAAG	AACCTTTTTTC TTGGAAAAAG	TCATTAGGCC AGTAATCCGG	TACAACATAG ATGTTGTATC	GACATCTCGG CTGTAGAGCC
181	ATAGAATTTTC TATCTTAAAG	CTTTTCTTTT GAAAAGAAAA	TGCTACTATA ACGATGATAT	AGCTGCTAAA TCGACGATTT	ATCCTCAGAA TAGGAGTCTT	CATCAGATTT GTAGTCTAAA
241	AGAAATGTTT TCTTTACAAG	TTATTAGTGG AATAATCACC	TAGTGAGCAT ATCACTCGTA	TTGCTATTTT AACGATAAAG	CTACCACTAG GATGGTGATC	CTTACAAATA GAATGTTTAT
301	TAATAAGCAA ATTATTCGTT	GTAGACCCCA CATCTGSSST	CAGGCCAAAT GTCCSGTTTA	TCCTATTTGT AGGATAAACA	TCTACAGTCG AGATGTCAGC	AAAGGGAATT TTTCCCTTAA
361	TTTTAAAAAT AAAATTTTAA	TAATTTCCAC ATTAAAGGTG	TAAAGAGAAA ATTTCTCTTT	AATATATTAA TTATATAATT	CAATCAAATT GTTAGTTTAA	GACAGTCGAT CTGTCAGCTA
421	TTTAATTTCT AAATTAACCA	ATGTGTAAAT TACACATTAA	TTTTTCCCTC CAAAAGGGAG	ATTATTTATA TAATAAATAT	ACAATTCATA TGTTAAGTAT	CTACAATTTA GATGTTAAAT
481	ATTTAGTAAA TAAATCATT	CATTTTTGTA GTAAAAACAT	GACCATATTT CTGGTATAAA	AAAACAAAGA TTTTGTTTTCT	TACTGAAAGT ATGACTTTCA	TAATATAAAC ATTATATTTG
541	TTAGTGCATG CTTCACGTAC	CTCTCTGTAG GAGAGACATC	GCCACAGCCA CGGTGTCCGT	TAACCTGTAA ATTGGACATT	GCACAGAAAA CGTGTCTTTT	ATTTGTTCTG TAAACAAGAC
601	TTACTCTAAA AATGAGATTT	CATCTACACT GTAGATTTGA	GGCCAAATTC CCGGTTTAAAG	CAATGCTCGA GTTACGAGCT	ATTTAACCCC TAAATTGGGG	GGGATATAAC CCCTATATTG
661	CTAGTAAATG GATCATTTAC	TGTCCTCTCT ACAGGAGAGA	GTCAAGGTGG CAGTTCCACC	GCATGTCACA CGTACAGTGT	GAATACAGAA CTTATGTCTT	CAATCAATGG GTTAGTTACC
721	TATTCATAAA ATAAGTATTT	GTTTTAAGAA CAAAATTCTT	AATGATTCTA TTACTAAGAT	CACATGTAAA GTGTACATTT	ACCCACTATA TGGGTGATAT	ACTTTTTTACA TGAAAAATGT

68/130

FIGURE 44B

781 TTGGGGGAGA GAAAAAAGA GATAATTTT ACCTTACCTT ATTTCTCTCTG AAAACTTTCC
AACCCCTCT CTTTTTTTCT CTATTAAAA TGGAATGGAA TAAAGGAGAC TTTTGAAAGG

841 CATATCTGGC AATTACAATT TTCCCAGAGC AATTGATTTT CATGTCCCTT TCC
GTATAGACCG TTAATGTTAA AAGGGTCTTC TTAATAAAA GTACAGGGCA AGG

69/130

FIGURE 45A

	10	20	30	40	50	60
1	GATGCTATTT CTACGATAAA	GGGCAATTTT CCCGTTAAAG	TTATTGACAG AATAACTGTC	TTTTGAAATG AAAACCTTAC	TTAGGCTTTT AATCCGAAAA	ATCTCCATTT TAGAGGTAAA
61	TTTAGTACTT AAATCATGAA	AAATTTTCCA TTTAAAAGGT	ACATGGGTGT TGTACCCACA	TGCTTGTTAT ACGAACAATA	TTTATCAGTA AAATAGTCAT	TAAAATAGAA ATTTTATCTT
121	GAGTGGTTCT CTCACCAAGA	GTTCTGGAAT CAAGACCTTA	TTAGTATATA AATCATATAT	CATGAGTATC GTACTCATAG	TAGTGTATGT ATCACATACA	CAGCCATGAA GTCGGTACTT
181	AATGAACCTT TTACTTGGAA	TCAGATGTTT AGTCTACAAA	AACTTCAGGG TTGAAGTCCC	AACCTAATTG TTGGATTAAC	AGTCATTGCT TCAGTAACGA	CCAGACATTG GGTCTGTAAC
241	TTGCTTTGAA AACGAAACTT	CCCACTATAT GGGTGATATA	TNNNNNNNCT ANNNNNNNSA	CGGGCAATTA GCCCGTTACT	CTCAGTGTGG GAGTCACACC	CAAGGATACT GTTCCATATGA
301	ACTGCAGGCC TGACGTCCGG	TGTTTCTGGA ACAAAGACCT	AGGCACTGGA TCCGTGACCT	CTCCTCTGAT GAGGAGACTA	GCAAACCTTG CGTTTGAAAC	GCCAGGGACT CGGTCCCTGA
361	CCTTGATAGC GGAACATATC	TCTTAAATAG AGAACTTATC	ATGCTGCACC TACGACGTGG	AACACTCTCT TTGTGAGAGA	TTCTTTTCTC AAGAAAAGAG	TCTTTTCTCT AGAAAAAGAA
421	TATTCAATAT ATAAGTTATA	TAGACTACAA ATCTGATGTT	GCACTCTAAT CGTCAGATTC	GACTTCTCAG CTGAAGASTC	GGTTTCTAGC CCAAAGATCG	TCTCTCTCAT AGAGAGAGTA
481	TTACACACATG AAGTGTGTAC	CTTTCTTAGT GAAAGSATCA	AATCTCTACT TTAGAGATGA	CATATATCTT GTATATAGAA	ACTGCTACGC TGACGATGCG	TGGGGCCAGA ACCCCGGTCT
541	TAAACNNNNN ATTGNNNNNN	CTTCCATTTT GAAGGTAAAA	GTCTTTTATCT CAAAAATAGA	CTATTCTTCT GATAAGAAGA	TCCCCTTCTG AGGGGAAGAC	CTTTCATTAT GAAAGTAATA
601	TGAAACTTTT ACTTTGAAAG	TGCTTTTCAAT ACGAAAGTAA	ATTGAAACTT TAACCTTGAA	TCCCAGATTT AGGGTCTAAA	GTTCTGCTTA CAAGACGAAT	ACCTGGCATT TGGACCGTAA
661	GGAACCTGTTT CCTTGACAAA	CCTCTTCCCT GGAGAAGGGA	GTGCTGCTTT CACGACGAAA	CTCCCATTCG GAGGGTAACG	CATGTCCTTT GTACAGGAAA	TTTTTTTTTT AAAAAAAAAA
721	TTTTTTTTTT AAAAAAAAAA	TGAGACAGTG ACTCTGTCAC	TCACTCTGTT AGTGAGACAA	GCCCAGGCTG CGGGTCCGAC	GAGTGCAATG CTCACGTTAC	GTGCAATCTT CACGTTAGAA

70/130

FIGURE 45B

781 GGCCACTGCA ACCCCGACTC CGGGTTCAAG TGATTCTCTA CCTGCCTCAG CCTCCTGAGT
CCGGTGACGT TGGGGCTGAG GCCCAAGTTC ACTAAGAGAT GGACGGAGTC GGAGGACTCA

841 AGCTGGGATT ACAGGTGCCA CCACTATGCC GGCTGATTTT GTATTTTAGT AGAGATGGGT
TCGACCCTAA TGTCCACGGT GGTGATACGG CCGACTAAAA CATAAAATCA TCTCTACCCA

901 TCACATGCAG ATCAGCTGTT CCGACTCTGA CCAGNNNNNN NNNNNNNNNN ATCAAAGTCA
ASTGTACCTC TAGTCGACAA GGCTGAGACT GGTNNNNNNN NNNNNNNNNN TAGTTTCAGT

961 GCCAAAGTGC TAGGCTTAGA GTAATTGTGT AATTTCCACA CAAGTGCAAC CTAGTGTAAT
CGGTTTCACG ATCCGAATCT CATTAAACACA TTAAAGGTGT GTTCACGTTG GATCACATTA

1021 GGGTCAAGAA TGTNNNTATG AATGTCTCGA ACGTTAGTAA CTAATAACAA GTAGTTAGTT
CGGAGTTCTT ACANNNTATC TTACAGAGCT TCGAATCATT GATTATTGTT CATCAATCAA

1081 TATAGATGTA TCCTAGTATG TAGCA
ATATCTACAT AGGATCATA ATCGT

71/130

FIGURE 46A

	10	20	30	40	50	60
1	CACAAAAAAA GTGTTTTTTT	GATTATTAGC CTAATAATCG	CACAAAAAAA GTGTTTTTTT	CCTTGAAGTA GGAAC TTCAT	ACGCATTAAA TGC GTAATTT	ATGTTAATGG TACAATTACC
61	ATTCAC TTTA TAAGTGAAAT	TTGAGCATCT AACTCGTAGA	GCTCATAATA CGAGTATTAT	CTTTAATGAG GAAATTACTC	TGCAAAGTGC ACGTTTCACG	TTTGAATATA AACTTATAT
121	ATACGTCATT TATGCAGTAA	TAAACCTTAC ATTTGGAATG	CATAATTCTG GTATTAAGAC	AGGAATTGCT TCCTTAACGA	ACCTCCACTT TGGAGGTGAA	CACAGATGGG GTGTCTACCC
181	GCACAGGAGG CGTGTCTCTC	CTTAGATAAC GAATCTATTG	ATGCCCAAAG TACGGGTTTC	TCATGCTTCT AGTACGAAGA	AGTAAATGGA TCATTTACCT	TATAATTAAG ATATTAATTC
241	ATTCAAATTA TAAGTTTAAT	TTGATAAGAA AACTATTCTT	TTTGATCTGC AACTAGACG	CTTACCAATA GAATGGT CAT	TCTAGTAGTA AGATCATCAT	AATCTAAAAG TTAGATT TTC
301	CGCTTTCCAG GCGAAAGGTC	AGCATGTGCT TCGTACACGA	GTTGATAGAG CAACTATCTC	CTTGATGTCT GAACTACAGA	AACTCTCTGA TTGAGAGACT	AATTTTCCAT TTAAAAGGTA
361	TCTTATTTGT AGAATAAACA	CTCACTGGTA GAGTGACCAT	TATAGTTATT ATATCAATAA	TTTTACTACT AAAATGATGA	TTCATACACC AAGTATGTGG	TACTAAGAAG ATGATTCTTC
421	ACAGGAGGAT TGTCCTCCTA	CAAAGATAGG GTTTCTATCC	ATTTCAATTA TAAAGTAAAT	GAATGGCTAA CTTACGGATT	AGCTTCACGT TCGAAGTGCA	ATTTTAATTC TAAAATTAAG
481	AGAATAAGAT TCTTATTCTA	TCAGGCAGAC AGTCCGTCTG	CACCAGTATA GTGGTCATAT	TCCCATGGTC ACGGTACCAG	CCTGGTTATC GGACCAATAG	TTTCAGCAGG AAAGTCGTCC
541	TGACCGAGAA ACTGGCTCTT	AGAAAACATG TCTTTTGTAC	GTAATGTTTA CATTACAAAT	TGAAATGGTG ACTTTACCAAC	GGTTCTTGTA CCAAGAACAT	GTTTCACTTC CAAAGTGAAG
601	AACATATCTG TTGTATAGAC	CCTTTACTGT GGAAATGACA	ATTAAGATGA TAATTCTACT	TGGATTAACT ACCTAATTGA	TATTCTTGAT ATAAGAACTA	ATGGGCATGT TACCCGTACA
661	AAAACAATAT TTTGTGTTATA	ACTTTTACTA TGAAAATGAT	AACAGCTACA TTGTCGATGT	GAGAGACAAA CTCTCTGTTT	TGTGTTTCCA ACACAAAGGT	GACAAACTTA CTGTTTGAAT
721	AGAGACTGAG TCTCTGACTC	TGTTCAAAC T ACAAGTTTGA	GAATAATCTC CTTATTAGAG	GACCTTAATT CTGGAATTAA	GTAAC TATAT CATTGATATA	TTTATGAAAT AAATACTTTA

72/130

FIGURE 46B

781 CCAGCTGTAA GGCAAAACAG ACTCTTGGCT ACACGGCATT TGTCTGTTAA TGATACTCAA
GGTCGACATT CCGTTTTGTC TGAGAACCGA TGTGCCGTAA ACAGACAATT ACTATGAGTT

841 COTTAACCGT CACTTAATAA TGCTGAATAA TGTCATTAAT CTGAGATGTT AGTATGATCA
GGAATTGGCA GTGAATTATT ACGACTTATT ACAGTAATTA GACTCTACAA TCATACTAGT

901 ATGGGAATCA CTGCTGAGCT CTCGAAGCCC
TACCCTTAGT GACGACTCGA GAGCTTCGGG

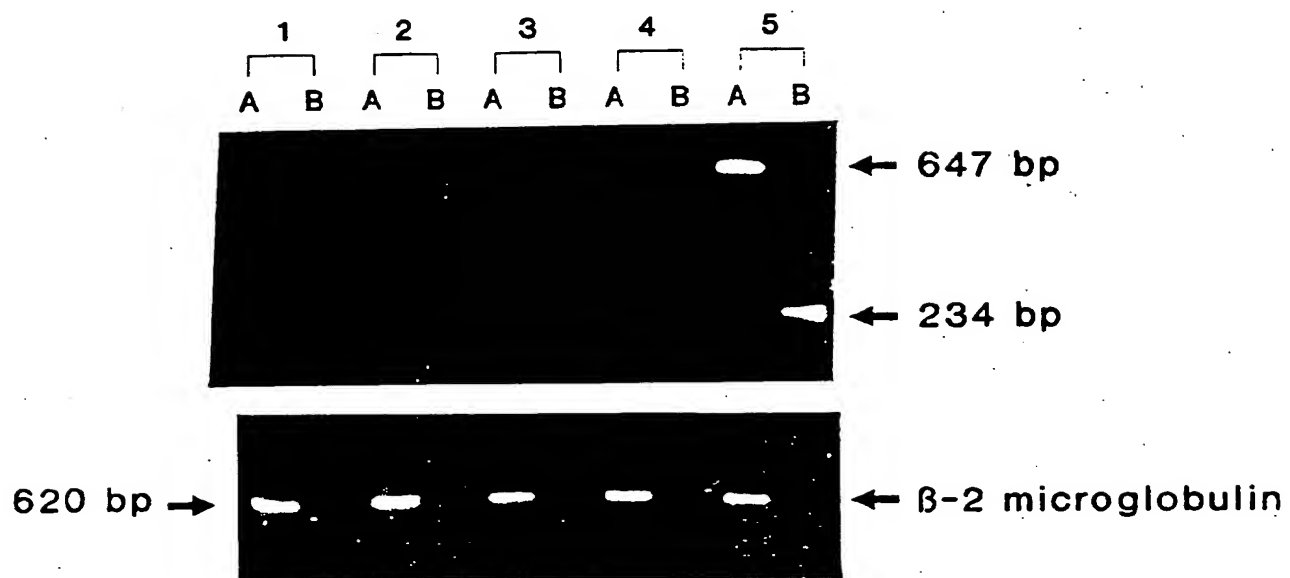
74/130

FIGURE 47B

CCA ACT GAA GAC TTC TTT AAA TTG GAA CAG GAC ATG AAA AAT TTC TCT GAG AAA ATT GTA ATT GGC AGA TAT GGG AAA GTT TTC AGA 630
 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asp Gys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg 210
 Intron
 GGA AAT AAG GTT AAA AAT GCG CAG CTG GCA GCG GCG AAA GGA GGC ATT CTG TAC TCC GAC CCT GCT GAC TAC TTT CCT CCT GCG GTG AAG 720
 Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gln Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys 240
 TCC TAT CCA GAT GAT TGG AAT GTT CCA GGT GAT GTC CAG CGT GGA AAT ATC CTA AAT CTG AAT GGT GGA GAC CCT CTC ACA CCA 610
 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Val Gln Arg Gln Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro 270
 GGT TAC CCA GCA AAT GAA TAT CCT TAT ACG CGT GCA ATT GGA GAG CCT GTT GGT CTT CCA AGT ATT CCT CAT CCA ATT GGA TAC TAT 900
 Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Gln Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr 300
 Intron
 GAT GCA CAG AAG CTC CTA GAA AAA ATG GGT GCG TCA CCA CCA GAT AAT AAG TGT ATA GGA AGT CTC AAA GTG CCG TAC AAT GTT GGA 990
 Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly 330
 CCT GGC TTT ACT GGA AAC TTT TCT ACA CAA AAA GTC AAG ATG CAC ATC CAC TCT AAT AAT GAA GTG ACA AGA ATT TAC AAT GTG ATA GGT 1080
 Pro Gly Phe Thr Gly Asn Phe Ser Thr Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Gln Val Thr Arg Ile Tyr Asn Val Ile Gly 360

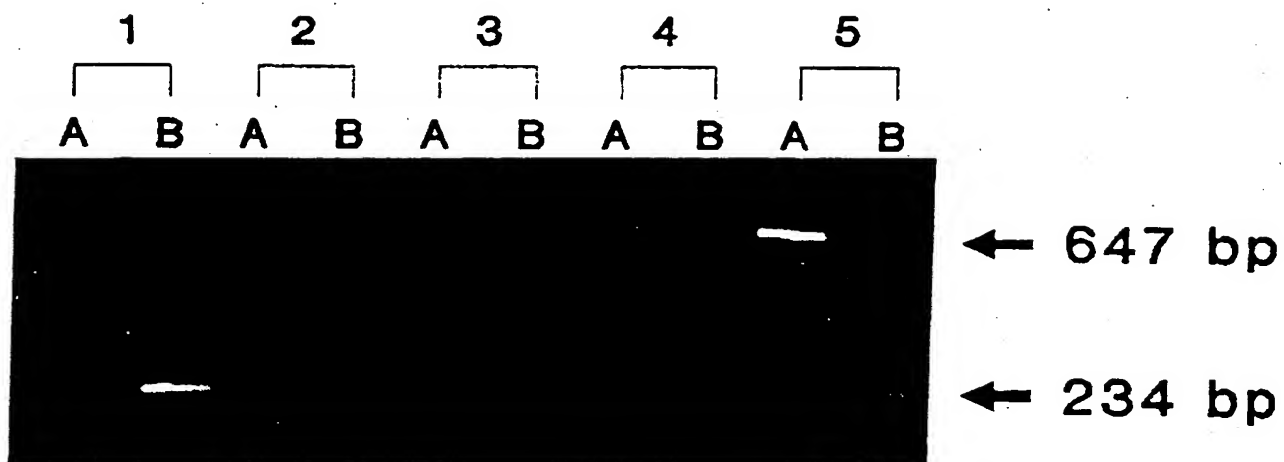
77/130

FIGURE 48



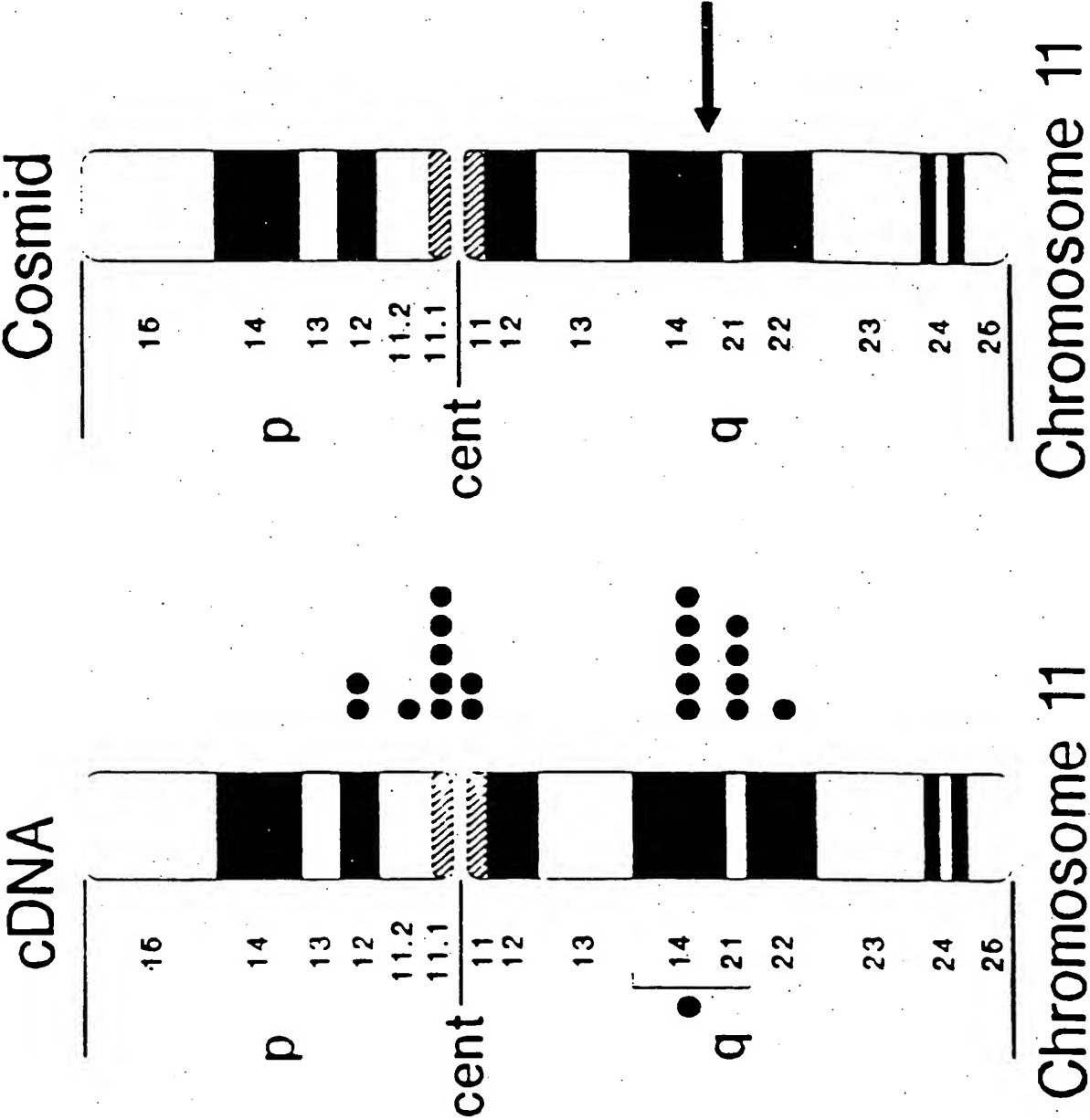
78/130

FIGURE 49



79/130

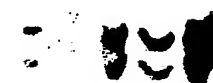
FIGURE 50



80/130

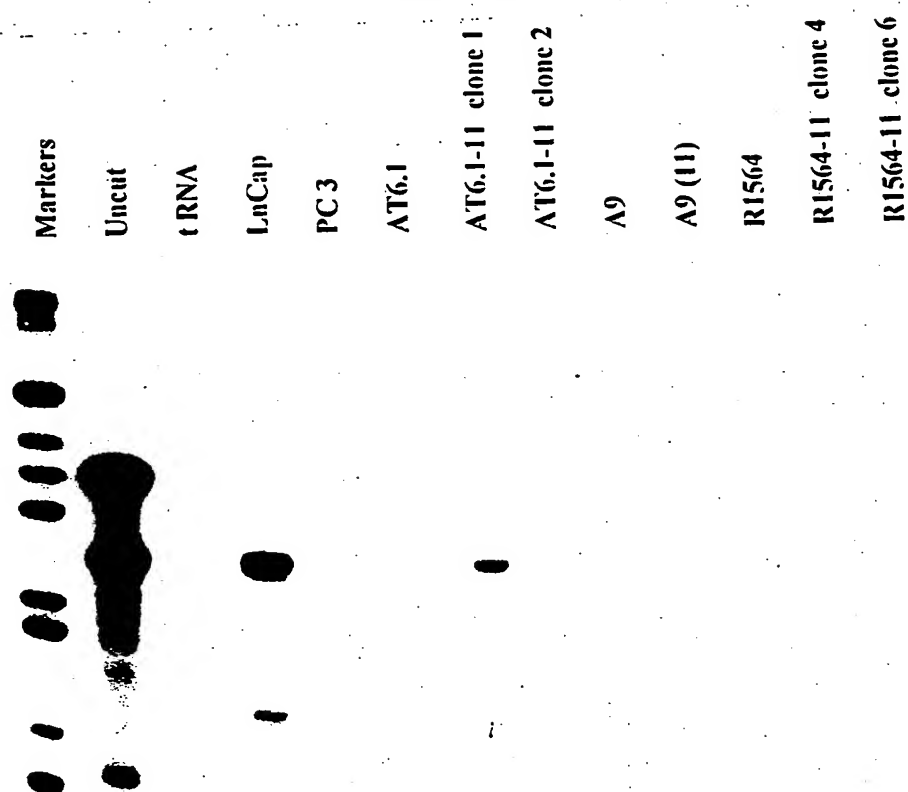
FIGURE 51

♂ ♀ M H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y



81/130

FIGURE 52



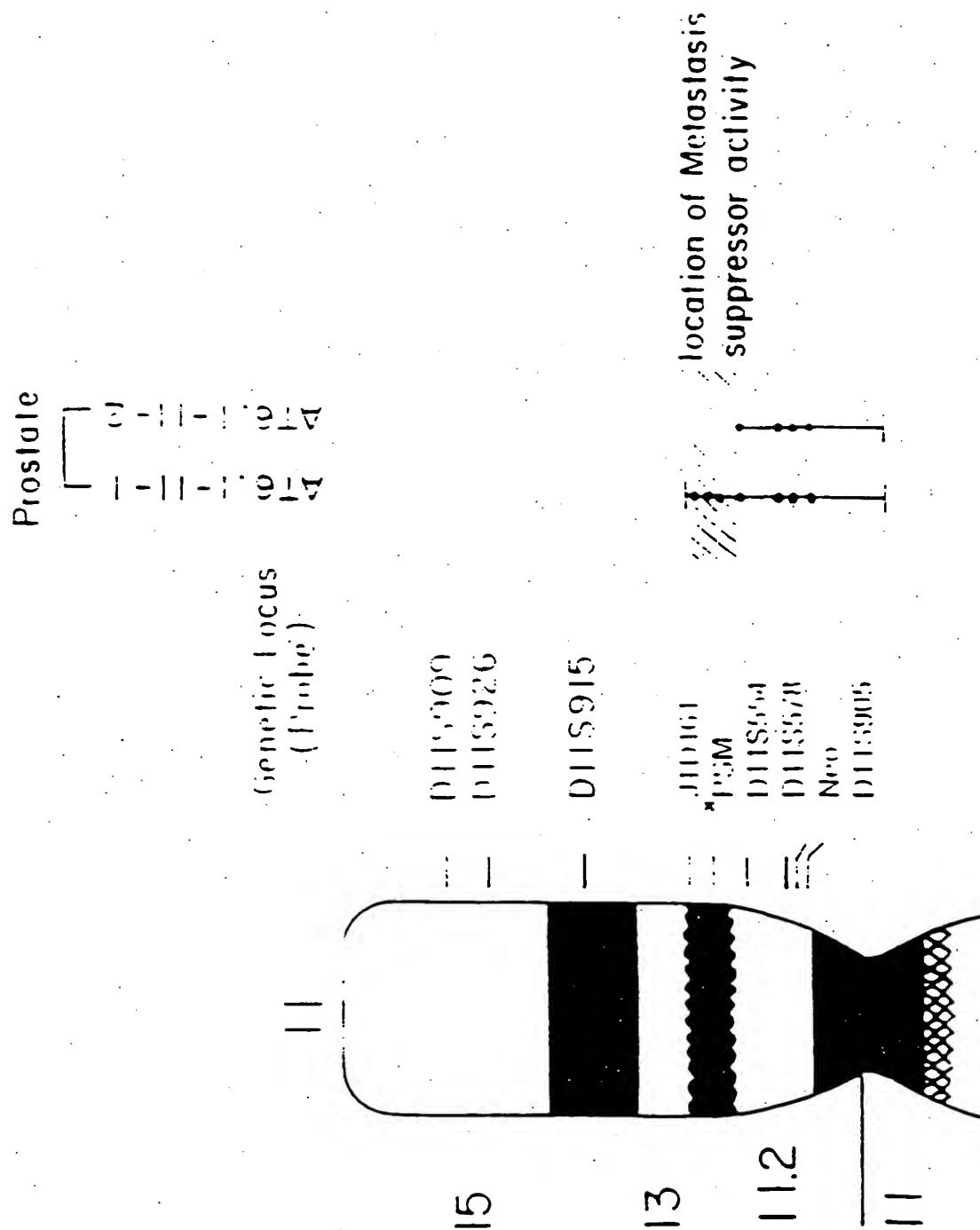
82/130

FIGURE 53

TISSUE/CELL LINE	CANCER CELL TYPE	PSM DNA	PSM RNA
HUMAN PROSTATE	N.A.	+	+
HUMAN MAMMARY	N.A.	+	-
AT6.1	RAT PROSTATIC ADENOCARCINOMA	-	-
AT6.1-11-CL1	"	+	+
AT6.1-11-CL2	"	-	-
R1564	RAT MAMMARY ADENOCARCINOMA	-	-
R1564-11-CL2	"	+	-
R1564-11-CL4	"	+	-
R1564-11-CL5	"	+	-
R1564-11-CL6	"	+	-
A9	MOUSE FIBROSARCOMA	-	-
A9(11)	"	+	-

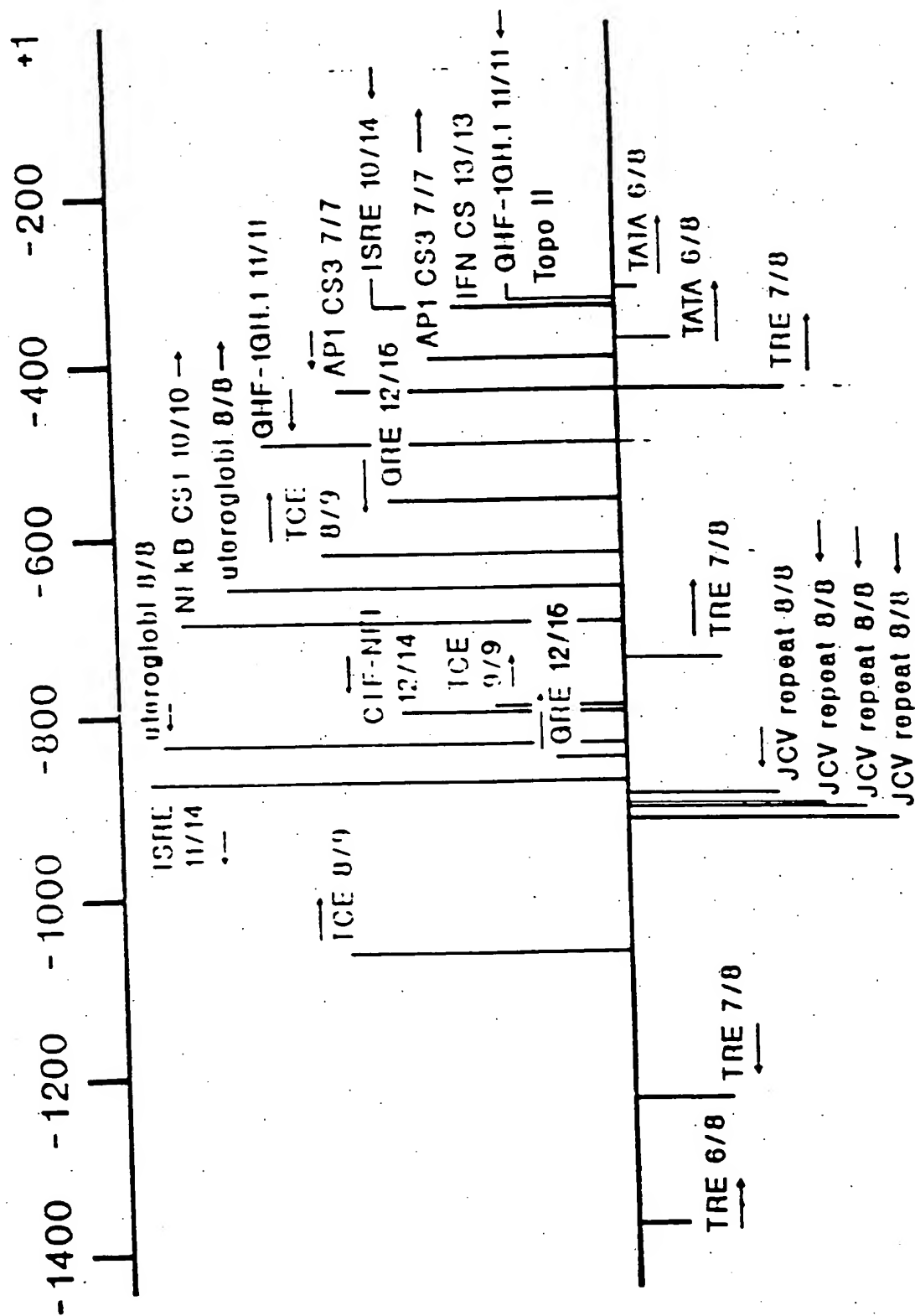
83/130

FIGURE 54



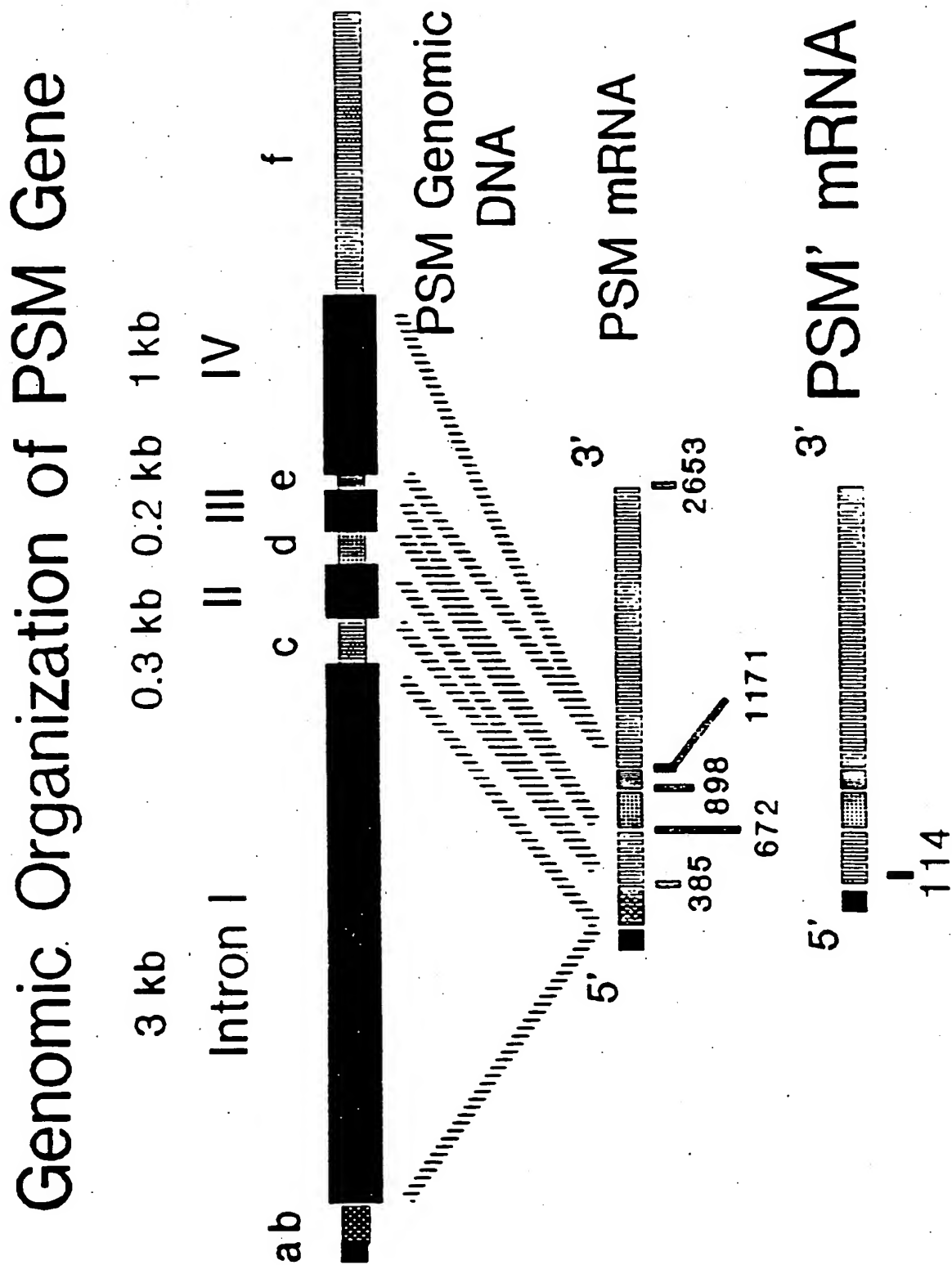
84/130

FIGURE 55



85/130

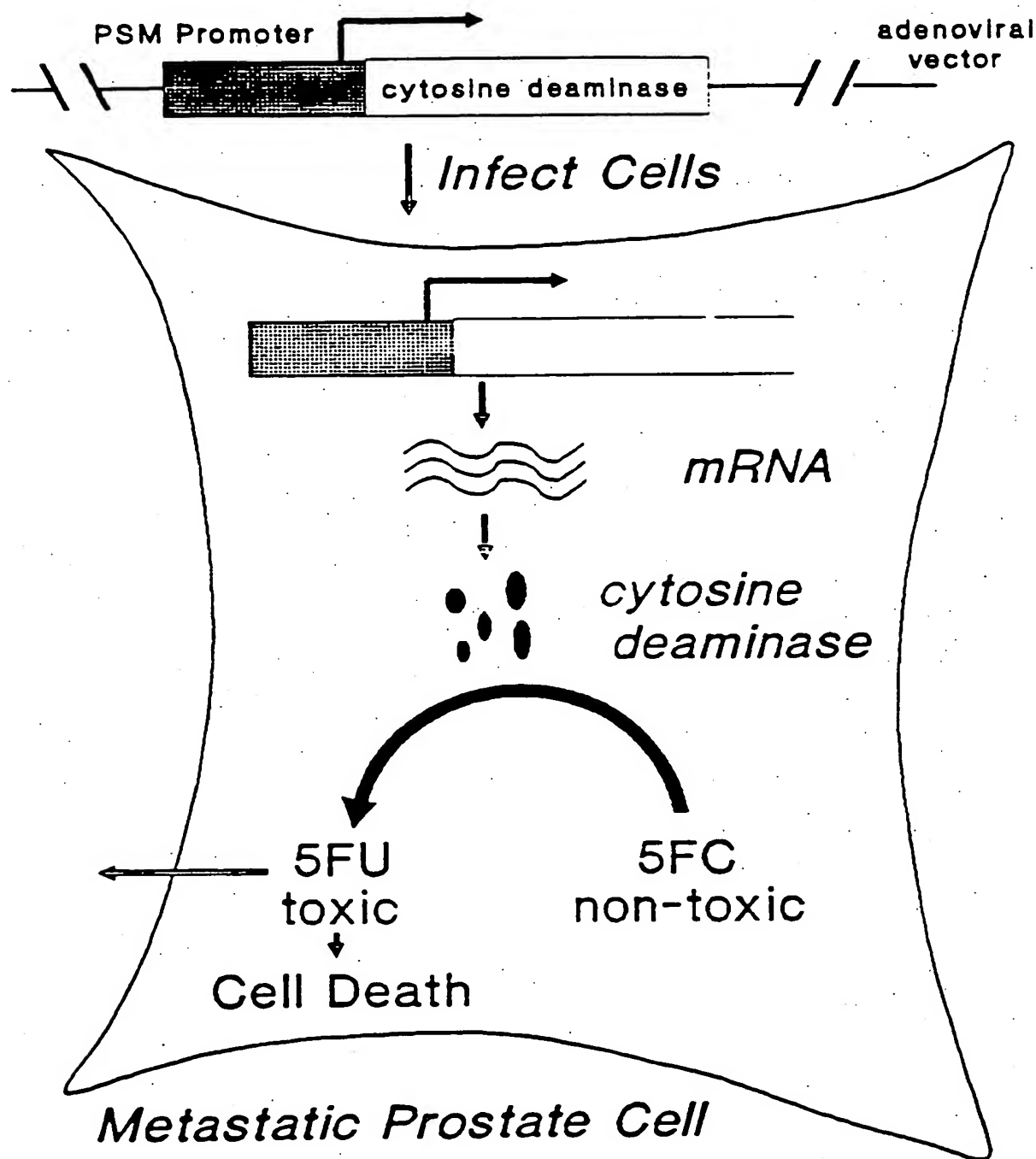
FIGURE 56



86/130

FIGURE 57

Prostate Specific Promoter: Cytosine Deaminase Chimera



87/130

FIGURE 58A

	10	20	30	40	50	60
1	GCGCCTTAA	AAAAAAAAAC	TTTCTTGGAA	AATGTCCAGC	TCTTGCTTAA	ATATAAAAT
	CGCGGAATTT	TTTTTTTTTG	AAAGAACCTT	TTACAGSTCG	AGAACGAATT	TATATTTTAA
61	GAAAGGAAGA	AAGAGACTCT	CCTCTCTCCA	CTCCTATAAT	TATGAGGAAC	TTTTATTCAA
	CTTTCCTTCT	TTCTCTGAGA	GGAGAGAGST	GAGGATATTA	ATACTCCTTG	AAAATAAGTT
121	CTCTGAAATT	CTATACAATC	TCTACAATAC	TCTACTGAAT	AAAAGCAGAG	CAGAAAAAGC
	GAGACTTTAA	GATATGTTAG	AGATGTTATG	AGATGACTTA	TTTTCGTCTC	GTCTTTTTTCG
181	TGCGCTTTTT	TTCCATAGTC	GGGAATGCTT	GTCATCAGTG	TAAATCACCA	CGCGCGCCTT
	ACCGGAAAAA	AAGGTATCAG	CCCTTACGAA	CAGTAGTCAC	ATTTAGTGTT	GGCGCGGGAA
241	TTTCCTAAAG	AATATGATTG	TTATTAATAA	ACATGTAGGG	TATTATCCTC	CACTTACATT
	AAAGGATTTG	TTATAATAAC	AATAATTATT	TGTACATCCC	ATAATAGSAG	GTGAATGTAA
301	ACAAAAACCAT	TTTTTAAAGC	CGGGCGTGGT	GCCTCACGCC	TSTAATSCCA	GCACTTTGGG
	TSTTTTGGTA	AAAAATTTTG	GCCCCGACCA	TGAGTGCGG	ACATTAGGGT	CGTGAACCC
361	AGGCCCCAGAC	AGGCGGATCA	CGAATCTGAG	AAATCGAGAC	CATCCTGGCC	AACATGGTGA
	TCCGGSTCTG	TCCCTCTAST	GCTTCAGCTC	TTTAGCTCTG	GTAGGACCGG	TGTACCACT
421	AACCCCATCT	CTACTAAAAA	TACAAAAATF	ACCTGGGCGT	GGTGGCGGGC	TCCTGTAGTC
	TTGGGSTAGA	GATGATTTTT	ATTTTTTTAA	TGACCCCGCA	CCACCGCCCG	AGGACATCAG
481	CGAGCTACTC	AGGAGGCTGA	GGTAGGAGAA	TGCTTTGAAC	CGGGGAGGCG	GAGGTTGCAG
	GGTGGATTAAG	TCTTCGACT	CGCTCTCTTT	AGCGAACTTG	GCCCCCTCCG	CTCCAACGTC
541	TCAGCCCAAG	TAGCGGCACT	CGACTGGAGC	GTGGTGACAG	AGTGAGACTC	CCTCAAGAAA
	AGTCGGTTCT	ATCGCGSTGA	CGTACCTCTG	GACCACTGTC	TCACTCTGAG	GGAGTTCTTT
601	GAAAGGAAGG	GAAGGGAAAG	GGAAAGGAAG	GGAGGGGAAG	GGAGGGGAGG	GGAGGGGAGG
	CTTTCCTTCC	CTTCCCTTTC	CCTTCTCTCC	CCTCCCCTTC	CCTCCCCTCC	CCTCCCCTCC
661	AAAGAAAAGA	ATACTGGAAC	TTGTTGAAGG	CAGAGACTTT	ATTTTCATAT	CCCGGCTATG
	TTTCTTTTTCT	TATGACCTTG	AACAACCTTC	GTCTCTGAAA	TAAAAGTATA	GGGCCGATAC
721	TCTGGCTACT	GTCTTACGTA	ATAGATATAA	AATCAATCTT	GGTTGGATTA	ACCAGAAGAA
	AGACCGATGA	CAGAAATGCAT	TATCTATATT	TTAGTTAGAA	CCAACCTAAT	TGGTCTTCTT

88/130

FIGURE 58B

781 TGAGAAGATA TATTCTGGTA AGTTGAATAC TTAGCACCCA GGGSTAATCA GCTTGGACAG
 ACTCTTCTAT ATAAGACCAT TCAACTTATG AATCGTGGST CCCATTAGT CGAACCTGTG

841 GACCAGGTCC AAAGACTGTT AAGAGTCTTC TGACTCCAAA CTCAGTGCTC CCTCCAGTGC
 CTGGTCCAGG TTTCTGACAA TTCTCAGAAG ACTGAGGTTT GAGTCACGAG GGAGGTCACG

901 CACAAGCAAA CTCCATAAAG GTATCSTGTG CTGAATAGAG ACTGTAGAGT GGTACAAAAGT
 GTGTTGTTTT GAGGTATTTT CATAGGACAC CACTTATCTC TGACATCTCA CCATCTTTCA

961 AAGACAGACA TTATATTAAG TCTTAGCTTT GTGACTTCGA ATGACTTACC TAATCTAGCT
 TTCTGTCTGT AATATAATTC AGAATCGAAA CACTGAAGCT TACTGAATGG ATTAGATCGA

1021 AAATTTTCAST TTTACCATGT GTAAATCAGG AAGAGTAATA GAACAAACCT TGAAGGGTCC
 TTTAAAGTCA AAATGGGTACA CATTAGTCC TTCTCATTAT CTTGTTTGOA ACTTCCCAGG

1081 CAATGGTGAT TAAATCAGGT GATGTACATA ACATGCATCA CTCATAATAA GTGCTCTTTA
 GTTACCACTA ATTTACTCCA CTACATGTAT TGTACGTAGT GAGTATTATT CACGAGAAAT

1141 AATATTAGTC ACTATTATTA GCCATCTCTG ATTAGATTTG ACAATAGGAA CATTAGGAAA
 TTATAATCAG TGATAATAAT CGGTAGAGAC TAATCTAAAC TGTATCTCTT GTAATCCTTT

1201 GATATAGTAC ATTCAAGATT TTGTTAGAAA GAGATGAAGA AATTCCTTTC CTTCTGCCC
 CTATATCATG TAAGTCCTAA AACAATCTTT CTCTACTTCT TTAAGGGAAG GAAGGACGGG

1261 TAGGTCACTCT AGGASTTGTG ATGGTTTCAAT GTTGACAAAT TAATTTTCCC AAATTTTCA
 ATCCAGTAGA TCCTCAACAG TACCAAGTAA CAACTGTTTA ATTAAGGAGG TTTAAAAAGT

1321 CTTTGCTCAG AAAGTCTACA TCGAASCACC CAAGACTGTA CAATCTAGTC CATCTTTTTC
 GAAACGAGTC TTTCAGATGT AGCTTCGTGG GTTCTGACAT GTTAGATCAG GTAGAAAAAG

1381 CACTTAACTC ATACTSTGGT CTCCCTTTCT CAAAGCAAAC TGTCTGCTAT TCCTTGAATA
 GTGAATTGAG TATGACACGA GAGGGAAAGA GTTTCGTTTG ACAAGCGATA AGGAACCTAT

1441 CACTCTGAGT TTTCTGCCCT TCCCTACTCA GCTGGCCCAT GGGCCCTAAT GTTCTCTCTC
 CTGAGACTCA AAAGACGGAA ACGGATGAST CGACCGGTA CCGGGGATTA CAAAGAAGAG

1501 ATCTCCACTG GGTCAAATCC TACCTGTACC TTATGTTTCT GTTAAAGGCA GTGCTTCCAT
 TAGAGGTGAC CCAGTTTAGG ATGGACATGG AATACCAAGA CAATTTTCTG CACGAAGGTA

1561 AAAGTACTCC TAGCAAATGC ACGCCCTCTC TCACGGATTA TAAGAACACA GTTTATTTTA
 TTTTCATGAGG ATCGTTTACG TGCCGGAGAG AGTGCCCTAAT ATTCTTGTGT CAAATAAAAT

1621 TAAAGCATGT AGCTATTCTC TCCCTCGAAA TACGATTATT ATTATTAAGA ATTTATAGCA
 ATTTCTGTACA TCGATAAGAG AGGGAGCTTT ATGCTAATAA TAATAATTCT TAAATATCGT

1681 GGGATATAAT TTGTATGAT GATTCTTCTG GTTAATCCAA CCAAGATTGA TTTTATATCT
 CCTATATTA AACATACTA CTAAGAAGAC CAATTAGGTT GGTCTAACT AAAATATAGA

1741 ATTACGTAAG ACAGTAGCCA GACATAGCCG GGATATGAAA ATAAAGTCTC TCCCTTCAAC
 TAATGCATTG TGTATCGGT CTGTATCGGC CCTATACCTT TATTTTCAAG ACGGAAGTTG

1801 AAGTTCCAGT ATTCTTTTCT TTCTTCCCTT CCCCCTCCCT CCGTTCCCTT CCCCCTCCTT
 TTCAAAGTCA TAAGAAAAGA AAGGAGGGGA GGGGAGGGGA GGGGAAGGGA GGGGAAGGGA

1861 CCGTTCCCTT TCCCTTCCCT TCTTTCTTGA GGGAGTCTCA CTCTGTCAAC AGGCTCCAGT
 GGGAAAGGGA AAGGAAGGGA AGAAAGAACT CCTCAGACT GAGACAGTGG TCCGAGGTCA

89/130

FIGURE 58C

1921 GCAGTGGCGC TATCTTGGCT GACTGCAACC TCAGCCTCCC CGGTTCAAGC GATTCTCCTG
 CGTCACCGCG ATAGAACCGA CTGACGTTGG AGGCGGAGGG GCCAAGTTCC CTAAGAGGAC

1981 CCTCAGCCTC CTGAGTAGCT GGGACTACAG GAGCCCCCCA CCACGCCCCAG CTAATTTTTC
 GGAGTCGGAG GACTCATCGA CCCTGATGTC CTCGGGCGGT GGTCGGGTC GATTAAAAAC

2041 TATTTTTAGT AGAGATGGGG TTTCACCATG TTGGCCAGGA TGGTCTCGAT TTCTCGACTT
 ATAAAAATCA TCTCTACCCC AAAGTGGTAC AACCGGTCCT ACCAGAGCTA AAGAGCTGAA

2101 CGTGATCCGC CTGTCTGGGC CTCCCAAAGT GCTGGGATTA CAGGCGTGAG CCACCACGCC
 GCACTAGGCG GACAGACCGG GAGGGTTTCA CGACCCTAAT GTCCGCACTC GGTGGTGGCG

2161 CGGCTTTAAA AAATGGTTTT GTAATGTAAG TGGAGGATAA TACCCTACAT GTTTATTAAT
 GCGAAAAATT TTTACCAAAA CATTACATTC ACCTCCTATT ATGGGATGTA CAAATAATTA

2221 AACATAATA TTCTTTAGGA AAAAGGGCGC GGTGGTGATT TACACTGATC ACAAGCATTTC
 TTGTTATTAT AAGAAATCCT TTTCCCGCG CCACCACTAA ATGTGACTAC TGTTCGTAAG

2281 CCGACTATGG AAAAAAAGCG CAGCTTTTTTC TGCTCTGCTT TTATTCAGTA GAGTATGTA
 GGCTGATACC TTTTCTTCGC GTCGAAAAAG ACGAGACGAA AATAAGTCAT CTCATAACAT

2341 GAGATTGTAT AGAATTCAG AGTIGAATAA AAGTTCCTCA TAATTATAGG AGTGGAGAGA
 CTCTAACATA TCTTAAAGTC TCAACTTATT TTCAAGGAGT ATTAATATCC TCACCTCTCT

2401 CGAGAGTCTC TTTCTTCCTT TCATTTTTAT ATTAAAGCAA GAGCTGGACA TTTTCCAAGA
 CCTCTCAGAG AAAGAAGGAA AGTAAAAATA TAAATTCOTT CTCGACCTGT AAAAGGTTCT

2461 AAGTTTTTTT TTTTAAAGGC GCCTCTCAAA AGGGGCGCGA TTTCTTCTC CTGGAGGCAG
 TTCAAAAAAA AAAAATTCGG CGGAGAGTTT TCCCGGCGCT AAAGGAAGAG GACCTCCGTC

2521 ATGTTGCTC TCTCTCTCGC TCGGATTGGT TCAGTGCACT CTAGAAACAC TGCTGTGGTG
 TACAACGGAG AGAGAGAGCG AGCCTAACCA ASTCAGCTGA GATCTTTGTG ACGACACCAC

2581 GAGAAACTGG ACCCCAGGTC TGGAGCGAAT TCCAGCCTGC AGGGCTGATA AGCGAGGCAT
 CTCTTTGACC TGGGGTCCAG ACCTCGCTTA AGGTCCGAGC TCCCGACTAT TCGCTCGGTA

2641 TAGTGAGATT GAGAGAGACT TTACCCCGCC GTGGTGCTTG GAGGGCGCGC AGTAGAGCAG
 ATCACTCTAA CTCTCTCTGA AATGGGGCGG CACCACCAAC CTCCCGCGCG TCATCTCTCT

2701 CACACACAGG CGGGGTCCCG GAGGSCCGGC TCTGCTCGCG CCGAGATGTG GAATCTCCTT
 GTGCTGTCCG CCCCCAGGCG CCTCCGSCCG AGACGAGCGC GGCTCTACAC CTTAGAGGAA

2761 CACGAAACCG ACTCGGCTGT GGGCACCAGC CGCCGCCCCC GCTGGCTGTG CGCTGGGGCG
 GTGCTTTGGC TGAACCGACA CCGGTGGCGC GCGGCGGGCG CGACCGACAC GCGACCCCGC

2821 CTGGTGCTCG CGGGTGCTT CTTTCTCCTC GGCTTCCTCT TCGGTAGGGG GCGGCTCGC
 GACCACGACC GCCCACCGAA GAAAGAGGAG CCGAAGGAGA AGCCATCCCC CCGCGAGCG

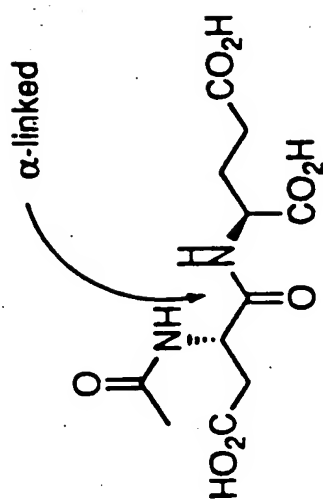
2881 GCAGCAAACC TCGGAGTCTT CCCCCTGGTG CCGCGGTGCT GGGACTCGCG GGTGAGCTGC
 CCTCGTTTGG AGCCTCAGAA GGGGCACCAC GCGGCCACGA CCTGAGCGC CCACTGAGC

2941 CGAGTGGGAT CCTGTTGCTG GTCTTCCCCA GGGGCGGGCA TTAGGGTCCG GGTAAATGTG
 GCTCACCTTA GACAAACGAC CAGAAAGGGT CCCCAGCGCT AATCCAGCC CCATTACAC

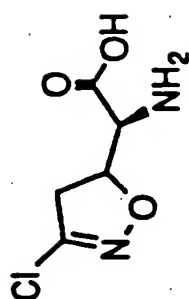
3001 GGTGAGCACC CCTCAG
 CCACTCGTGG GGAGCTC

90/130

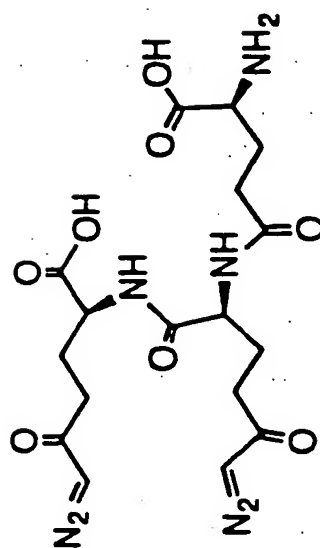
FIG. 59



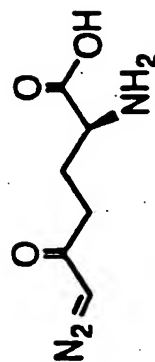
NAAG 1
N-acetylasparyl-L-glutamate



Acividin



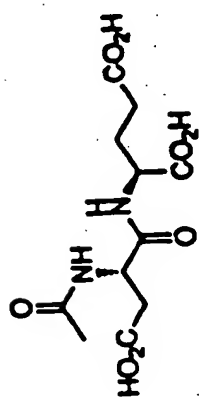
Azotomycin, becomes active by *in vivo* conversion to DON



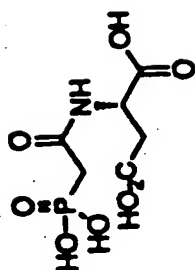
6-diazo-5-oxo-norleucine, DON

91/130

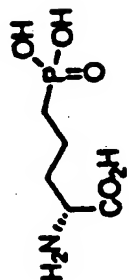
FIG. 60



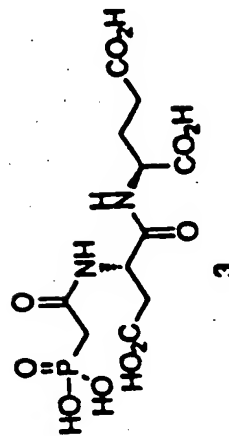
NAAG 1
N-acetyl-L-glutamate



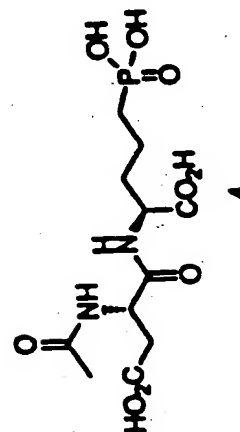
PALA 2
N-phosphonoacetyl-L-aspartate



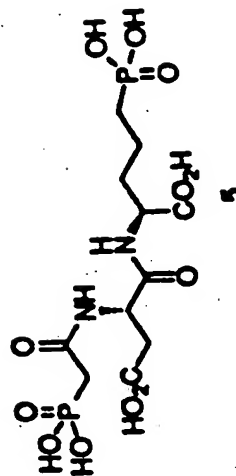
D-APV
L-Glu antagonist



3



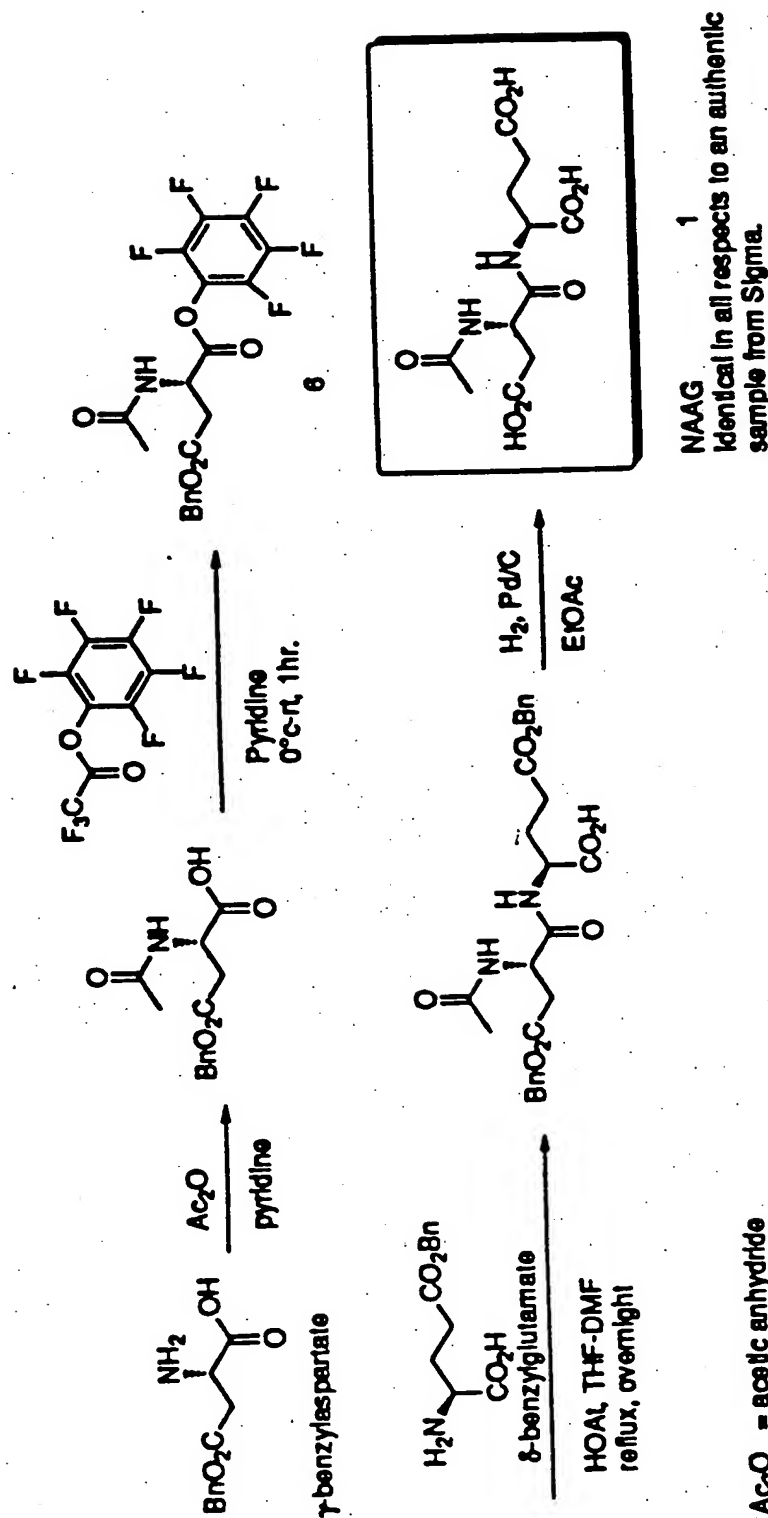
4



5

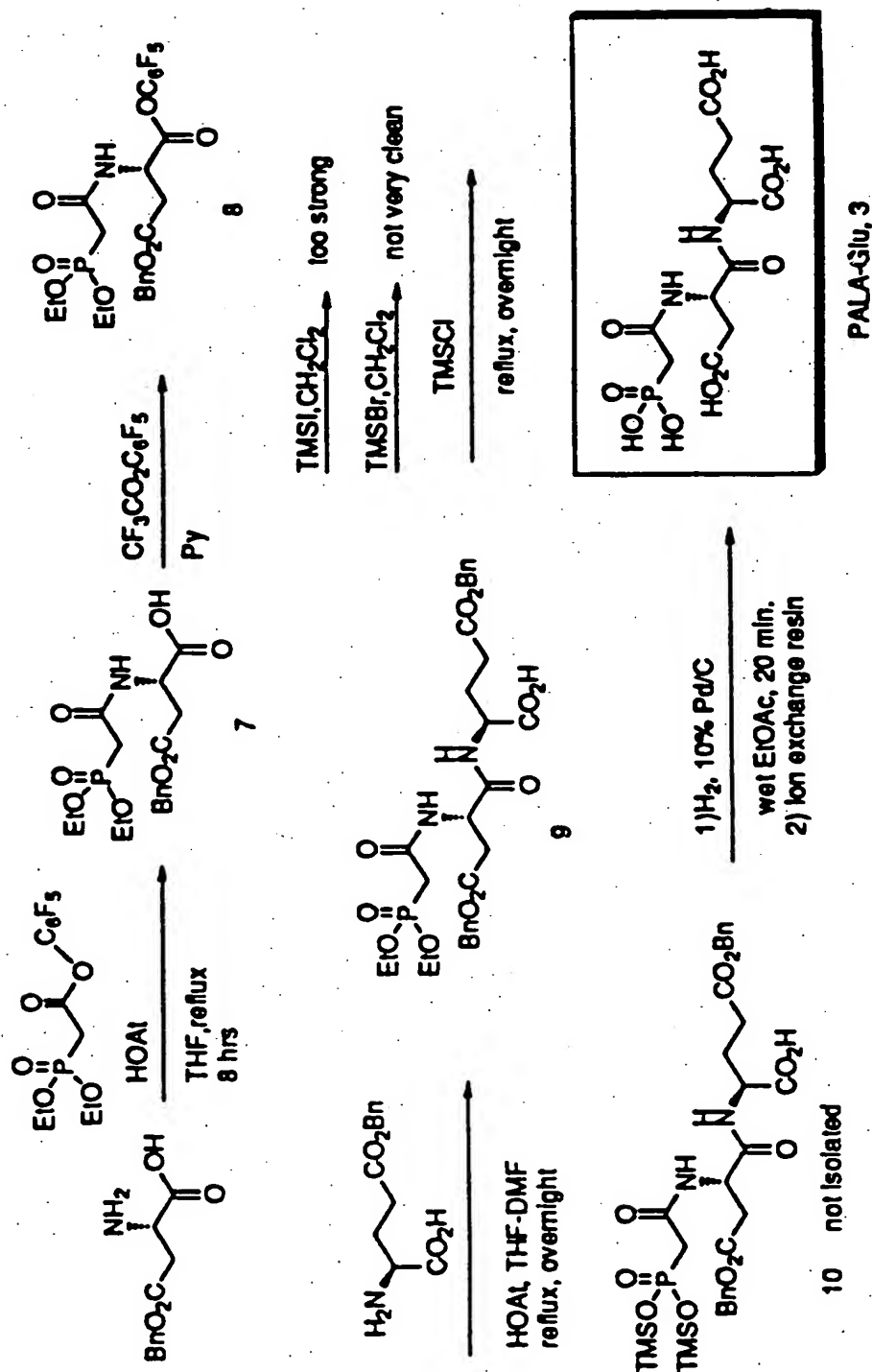
92/130

FIG. 61



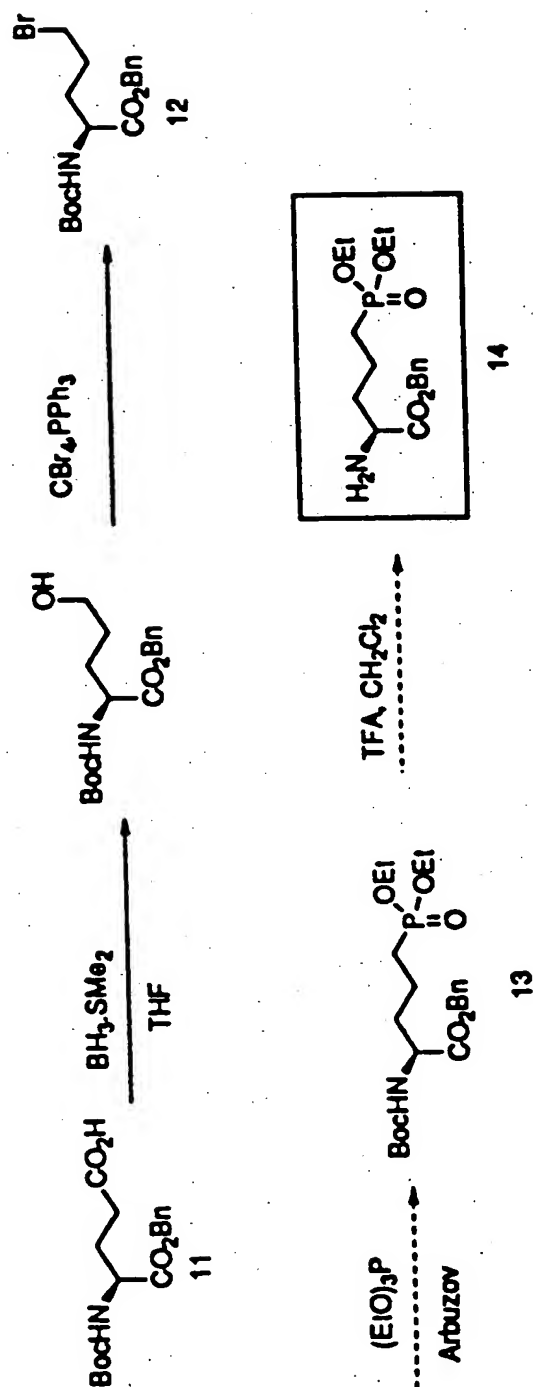
93/130

FIG. 62



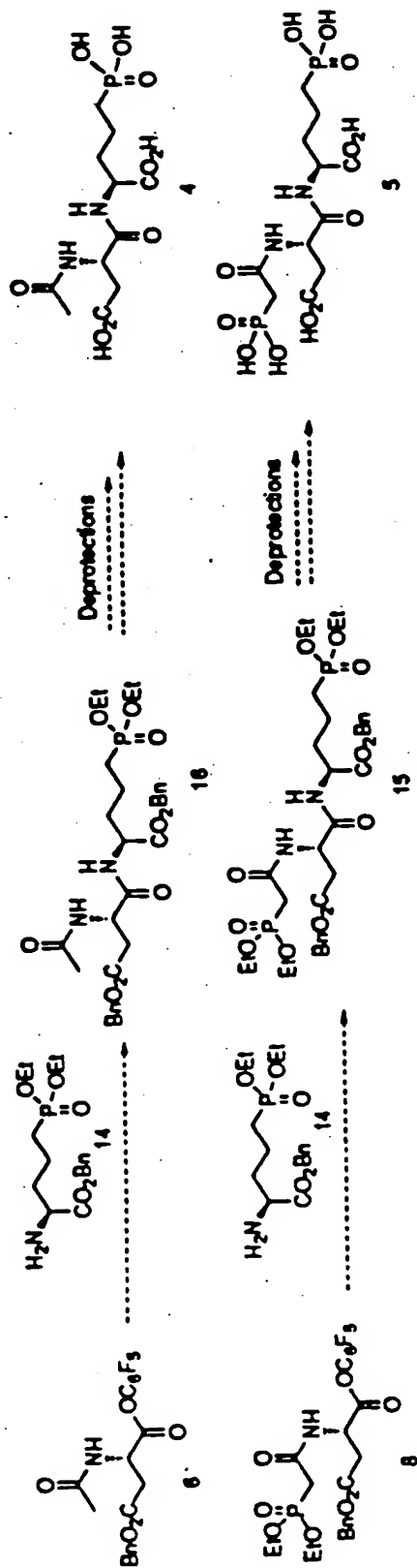
94/130

FIG. 63



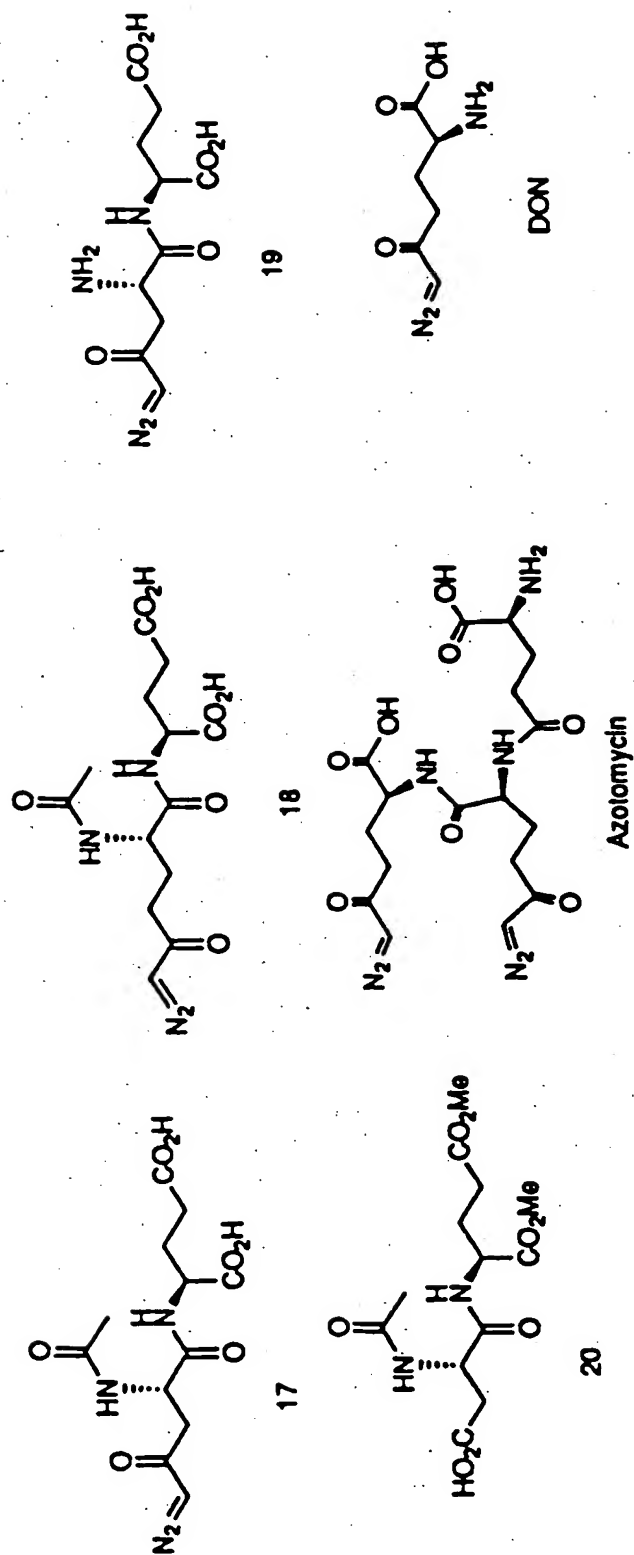
95/130

FIG. 64



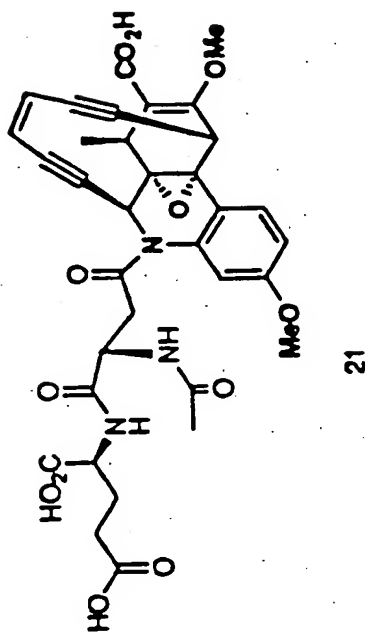
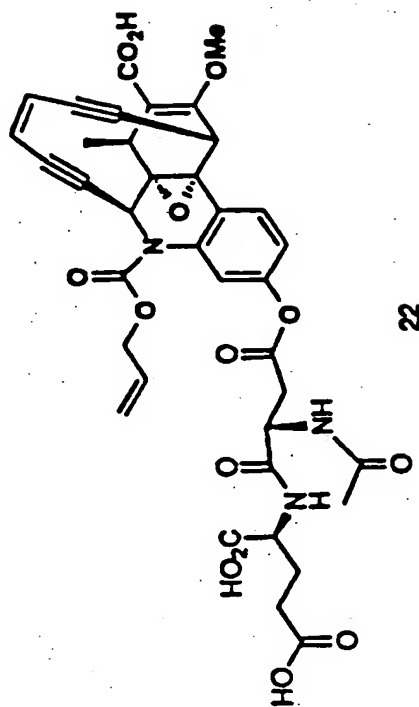
96/130

FIG. 65

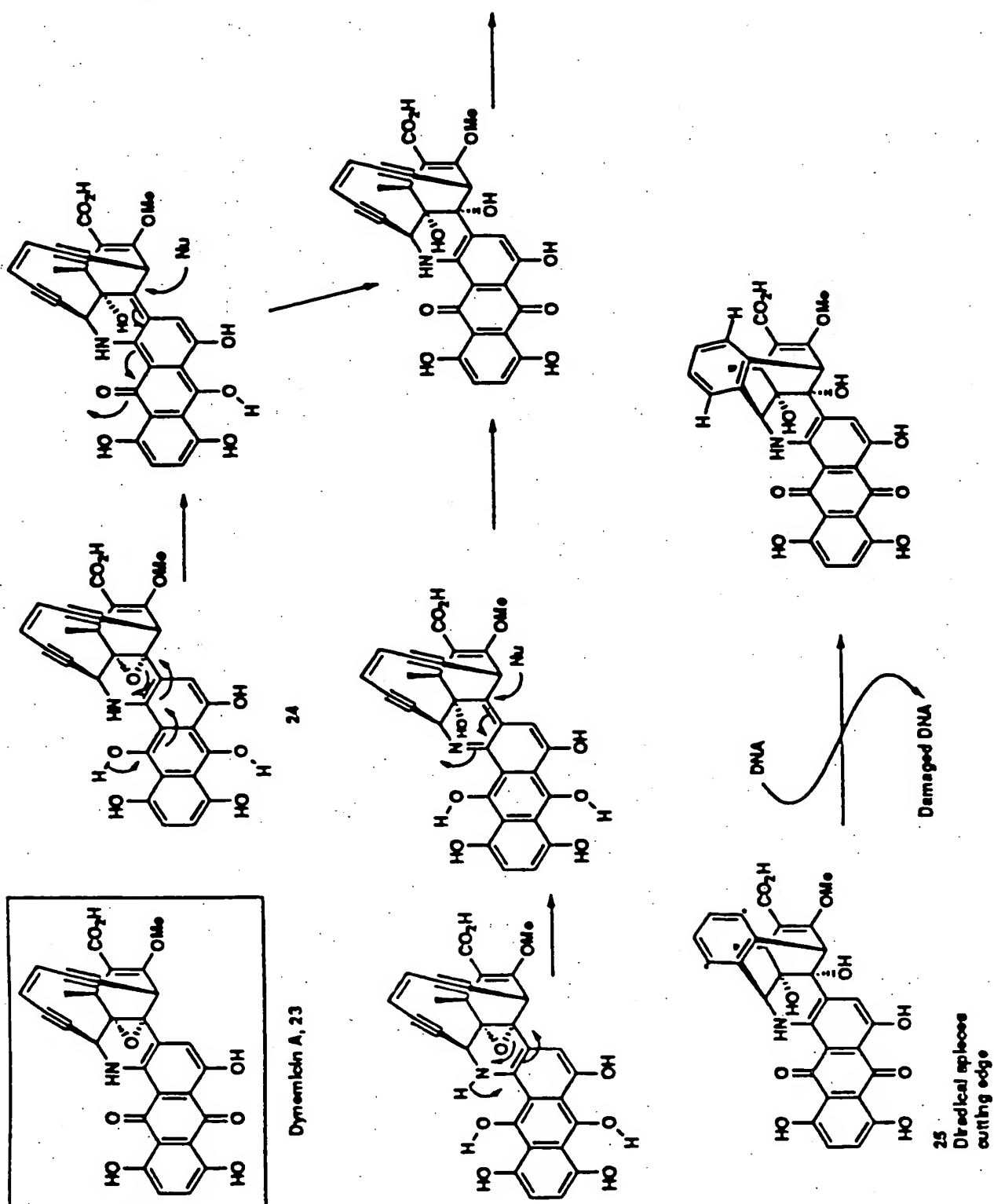


97/130

FIG. 66

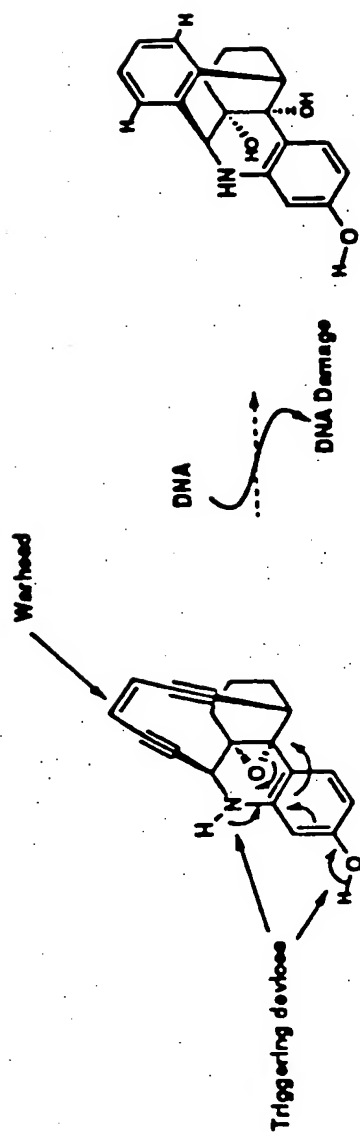


98/130

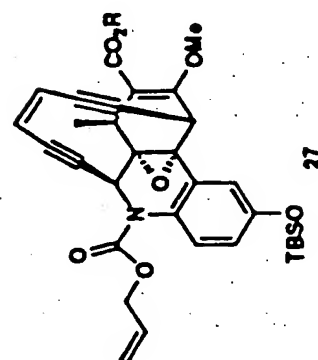
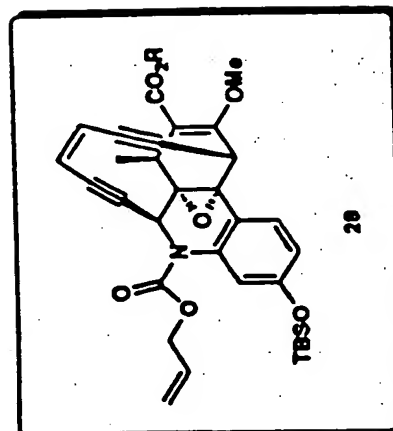


99/130

FIG. 68

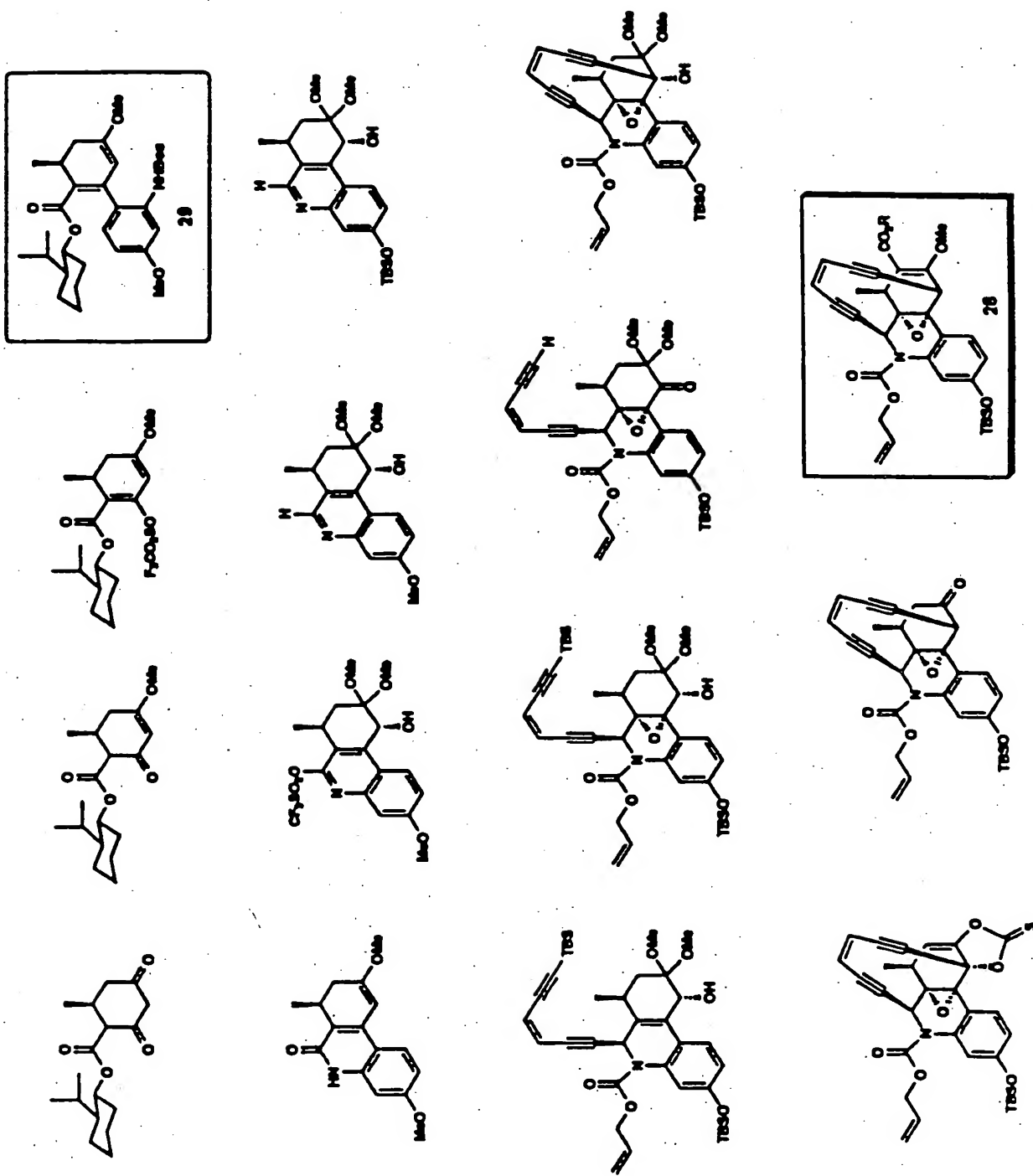


26
active at the nano to picomolar levels in different cell lines
readily rearranges when one or both
triggering devices are deprotected



100/130

FIG. 69



17 Steps for the optically active form 2

101/130

FIG. 70

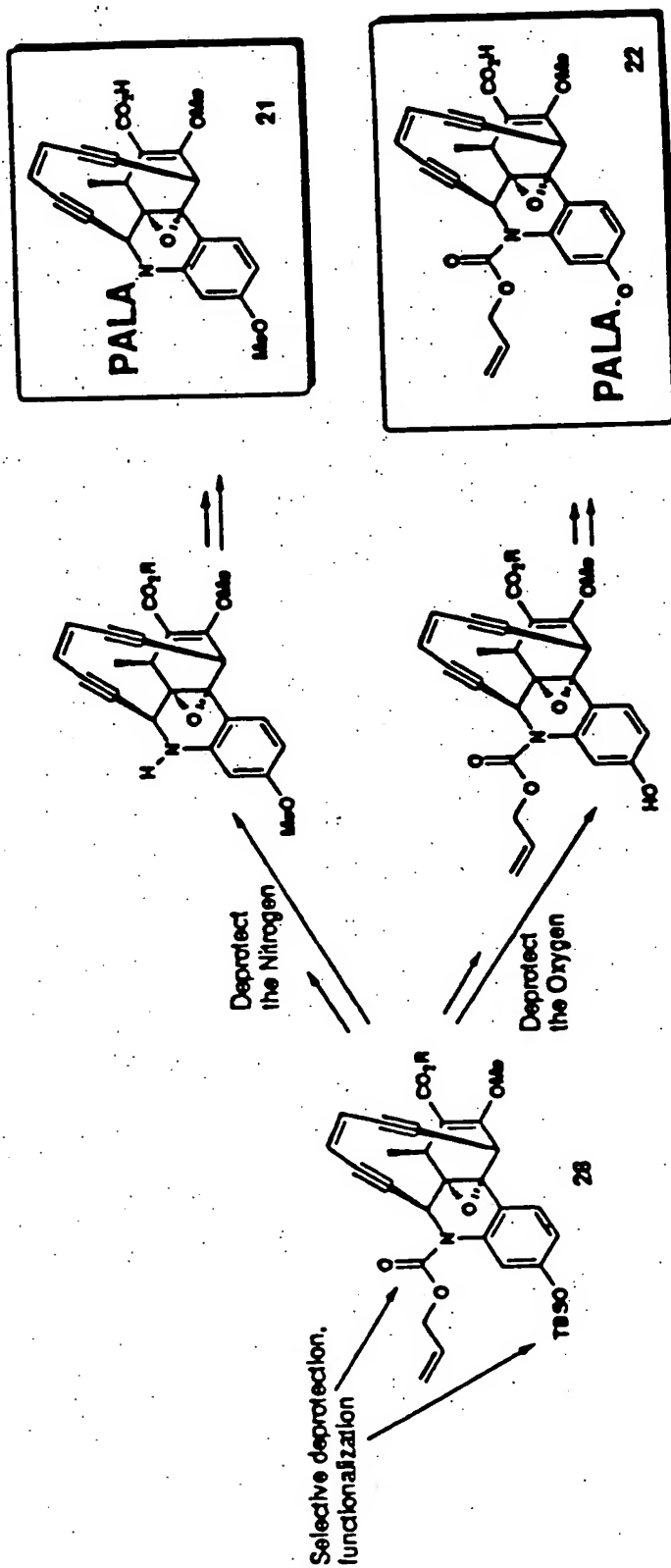
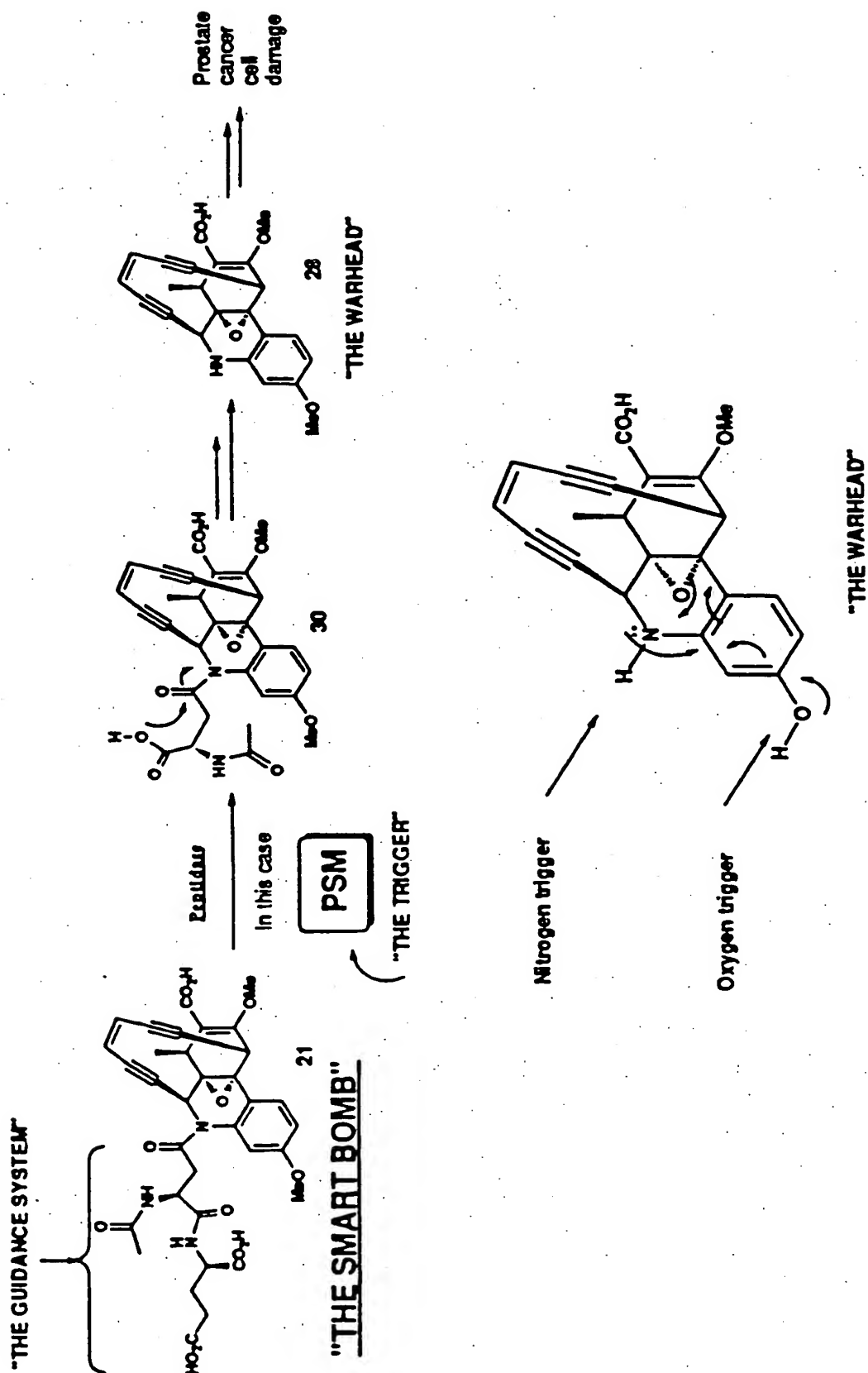


FIG. 71



103/130

FIG. 72A

	10	20	30	40	50	60
1	TAGGGGGCG	CCTCGGGGAG	AAACCTCGGA	GTCTTCCCCG	TGGTGCCGGC	GTGCTGGGAC
	NTCCCCCGC	GGAGGCGCTC	TTTGGAGCCT	CAGAAAGGGC	ACCACGGGCG	CACGACCCCTG
61	TCGCGGGTCA	GCTGCCGAGT	GGGATCCTGT	TGCTGGTCTT	CCCCAGGGGC	GGCGATTAGG
	AGCGCCAGT	CGACGGCTCA	CCCTAGGACA	ACGACCAGAA	GGGTCCCCG	CCGCTAATCC
121	GTGCGGGTAA	TGTGGGCTGA	GCACCCCTCG	AGTTAGGAGG	AGGTAGCTG	GGAAACGGTGC
	CAGCCCCATT	ACACCCCACT	CGTGGGAGC	TCAATCCTCC	TCCATCGAC	CCTTGCCACG
181	AGGGCTGAGT	TCTCGACAAG	CTGCTGGTAG	GACAGTCACT	CAGGTTGAGG	GTAGAAGCTGA
	TCCCGACTCA	AGAGCTGTTT	GACGACCATC	CTGTCAGTGA	GTCCAACCTC	CATCTTGACT
241	GAGAACCTGA	AAGTGGGCGT	AGGAAGGTC	CAAGTGCTGG	AGCCCTGCAA	GACAGAGGAA
	CTCTTGACT	TTGACCCGCA	TCCTTCCAG	GTTACGACC	TCGGGAGGTT	CTGTCTCCTT
301	GTCTTTT	TGCTTTTGT	TTGTTTGT	TTGTTTGT	TTGTTTGT	TGTTTGT
	CAAAAAA	ACGAAACAA	AACAAACAA	AACAAACAA	AACAAACAA	ACAAACAA
361	TTTTTTTACC	TCTCTGTGCA	TTCTTTCTTC	CTTGGAAAGTA	ACAGAGGCAA	GCTTGGGAAC
	AAAAAATGG	AGAGACACGT	AAGAAAGAG	GAACCTTCAT	TGTCTCCGTT	CGAACCCCTTG
421	TGTGTGAACC	AGGTCAGCAA	TCGACACAGG	TCCTTACCAG	CGGTCCTTTT	GCTGTTTTC
	ACACACTTGG	TCCAGTCTGT	AGACCTGTCC	AGAAATGGTC	GCCCAGNAAA	CGACAAAAAG
481	CTGGGTACTG	ATTTGCAGAC	TTGATCCAAC	TTTCTAAGAA	AAGCAGAACC	ACACAGGCAA
	GACCCATGAC	TAAACGTCTG	AAGTAGGTTG	AAAGATTCTT	TTCTCTCTGG	TGTGTCCGTT
541	GCTCAGACTC	TTTTATTAAA	TTCCAGTTT	GACTTTGCCA	CTTCTTAGTG	GCCTTGAACA
	CGAGTCTGAG	AAAAATAATT	AAGGTCAAAA	CTGAACGGT	GAAGATCAC	CGGAACCTTG

104/130

FIG. 72B

601 AGTACCGAG TCCCTCTCAG CGTTAGTTAC CCTATTTTAT GATGAGGATA ATATTATCTG
TCAATGGCTC AGGAGAGTC GCAATCAATG GGATAAATA CTACTCCTAT TATAATAGAC

661 CAAATTATTG GTAATAGTAA ATAATATAGC ATGTAAATCT CCTAGCACAG TACTGGGATT
GTTTAATAAC CATTATCATT TATTATATCC TACATTTAGA GGATCGTGTC ATGACCCCTAA

721 TTCGCCACTT TATTCTTCT TTTACCAAGA TACTCCTCAT TGGACTTTAA TACACAGGAC
AAGCGGTGAA ATAAAGAAGA AATCGTTCT ATGAGGAGTA ACCTGAAATT ATGTGTCCTG

781 TAGTCTAAGG TATCACGAGG TAGTCCACTC CTGCTCGGAA TTCTTGACCC TCTTTCGGGA
ATCAGATTCC ATAGTGGTCC ATCAGGTGAG GACGAGCCTT AAGAACTGGG AGAAAGCCCT

841 TTTAGAAGAA TAGGGCATGG ACCAGATGGG TTTAAACAAA TTCAATATCT TCCACTAGCT
AATCTTCTT ATCCCGTACC TGGTCTACCC AAATTGTGTT AAGTTATAGA AGGTGATCGA

901 TCACCTTGGG GTTGTAAAA GATTTTGA A CCACACACTG TGCTCATAAC AATCTTCATC
AGTGGAAACC CAACAATTT CTAAAACTT GGTGTGTGAC ACGACTATTG TTAGAAGTAG

961 TCTTAAAGG ATTTATCT TCCGTGATT GCCCTCACTC TCATCCCTGT ATCCCGTCT
AGAATTTTCC TAAATAAGA AGGACCATAA CGGGAGTGAG AGTAGGGACA TAAGGCACGA

105/130

FIG. 72C

1021 CAGTGGCTGA CACAGAAGAG TTCTTTATTG ATGTCGGCCC CCCACCCACT AGGATTCTCT
GTCACCGACT GTGTCTTCTC AAGAAATAAC TACAGGGCGG GGTGGGTGA TCCTAAGAGA

1081 GCTCTCCCTT CCCCTACAG GCCTCCATCC TCTTCATCCT GTTCATTTT CAGATCTCAG
CGAGAGGGGA GGGGATGTC CGGAGGTAGG AGAAGTAGGA CAAGTAAATA GTCTAGAGTC

1141 TTCAAGCATC TCGTCCTCAG TGTGGTGTTT CCTGATCCCT CACTCTAATC CAAGTCTTTC
AAGTTCGTAG AGCAGGAGTC ACACCACAAA GGACTAGGGA GTGAGATTAG GTTCAGAAAG

1201 TGTTTTATGC ACAGGTGGAA TCTTATTTC GTTGGCTCC AATCATGTAT TTTAATAAGC
ACAAATACG TGTCCACCTT AGAATAAAG CAAACGCAGG TTAGTACATA AAATTATACG

1261 ATGTATATAT GTATGTGCAT TTGTATGCAT GCGATTAGA ACTAGAATAA TTAATAATTG
TACATATATA CATACACGTA AACATACGTA CGCTAATTCT TGATCTTATT AATTATTAACT

1321 GAAAGCTCCA TGAAGCTGG TTGGGGACTA ATTTGTAACT TACTTTATTC CCAGATCCTG
CTTTCGAGGT ACTTTCGACC AACCCTGAT TAAACATTG ATGAATAAAG GGTCTAGGAC

1381 TAATTCTCT AAATAAACCC TGGATCTTG CCTATCTCC TTCAGGTAA AAGCCAACTG
ATTAAAGAGA TTTATTGGG ACCTTAGAAC GGAATAGAGG AAGTCCAATT TTCGGTTGAC

1441 CAAGGTCTAA TGACTGCAGG ATCTAGCTAT CCATTGTTT TGGCCGCCCTA TGGGTGCACT
GTTCCAGATT ACTGACGTCC TAGATCGATA GGTAAACAAAG ACCGGCGGAT ACGCACGTGA

1501 GGGTGTCTGG CAGAGAGGCT GGGTAATG TAGTTTCATT GTAGCTGTCT GACTTGGATT
CCCACAGACC GTCTCTCCGA CCCATTAACT ATCAAAGTAA CATCGACAGA CTGAACCTAA

1561 TCTCAGCCTT ACTTCACTGG AAACGCAAC TCTCACAGCA TTTTGTTTTA GTTTCAGAAT
AGAGTGCGGA TGAAGTGACC TTTGGTTTG AGAGTCTCTT AAAACAAAT CAAAGTCTTA

1621 CAGAGCAAT TAGAAGTCTG AATTCCTTC AACACTTGA AATAATTAT TTATTGAAA
GTCTCGTTTA ATCTTCAGAC TTAAGGAAG TTGTGAACCT TTATTAAATA AATAACTTT

1681 TATATTCATA ATTAATTCGT TATAAAATG TATTAAATGC TTATTTGAGT CAGCAGAGGA
ATATAAGTAT TAATTAGCA ATATTTTAC ATAATTAGG AATAAACTCA GTCGTCTCCT

106/130

FIG. 72D

1741 AGATAGAAAC TTTATGAAAG TAGAAGGTGG ATCTCCTTTT TGCCTTCATT TTCAGAACAT
TCTATCTTGG AATACTTTC ATCTTCCACC TAGAGGAAAA ACGGAAGTAA AAGTCTTGTA

1801 CTCGTTTACA CCCATTAGTT GAAACATTAA TGTCAATTTA TTTTCGTCCT GATTATCTCA
GAGCAANTGT GGGTAATCAA CTTTGTAATT ACAGTAAAT AAAAGCAGGA CTAATAGAGT

1861 TAAACATTT CTTAGAAATA CAGCAATACC TATCATTGAA GTTGGATAAG AAATATTTTG
ATTTGTAAA GAATCTTATT GTCGTTATGG ATAGTAACTT CAACCTATT TTTATNAAAC

1921 CAATTGGTTT GCAACTTAAA AATCTGTTTG CATGACTCTT TTTCAGTGAA AGTAGGCAAG
GTTAACCAAA CGTTGAATTT TTAGACAAAC GTACTGAGAA AAGTCACTT TCATCCGTTT

1981 AGAAATTAAA ATTCAGAAAT ATCTCACCTA ATGTCAGAGG TAATATTGAT AATTGTGTT
TCTTTAATTT TAAGTCTTTA TAGAGTGGAT TACAGTCTCC ATTATAACTA TTAAACACAA

2041 TTACAAATAA TACATACAAC AATAATGAAA AATAAGTCCT ATCTATAGGC TCGTATCTCA
AATGTTTATT ATGTATGTTG TTATTACTTT TTATTCAGGA TAGATATCCG AGCATAGAGT

2101 TGCCTATTTT TGGATGTATT TTTC
ACGGATAAAA ACCTACATAA AAAGT

107/130

FIG. 73A

10 20 30 40 50 60
1 TGAAAAATAC ATCAAAAATA GGCATCAGAT ACGAGCCCTAT AGATAGGACT TATTTTTTAT
ACTTTTTATG TAGTTTTAT CCGTACTCTA TGCTCGGATA TCTATCCTGA ATAAAAAATA
61 TATTGTTGTA TGTATTATTT GTAAACACA AATTATCAAT ATTACCTCTG ACATTAGGTG
ATNACAACAT ACATAATAAA CATTTTGTGT TTAATAGTTA TAATGGAGAC TGTAAATCCAC
121 AGATATTCTG AATTTTAATT TCTCTTGCTT ACTTTCACCTG AAAAGAGCTC ATGCAAAACAG
TCTATAAGAC TTAANAATTAA AGAGAAGGGA TGAAGGTGAC TTTTCTCTCAG TACGTTTGTC
181 ATTTTAAAGT TGCMAACCAA TTGCAAAATA TTTTCTTATC CAACCTCAAT GATAGGTATT
TAAAAATTCA ACGTTTGGTT AACGTTTAT AAAAAAATAG GTTGAAGTTA CTATCCATAA
241 GCTGTTAATT CTAAGATATG CATTAAATGT TTCAACTAAT GGGTGTCAAA CGAGATGTTT
CGACAATTAA GATTCCTATAC GTAATTAACA AAGTTGATTA CCCACAGTTT GCTCTACAAG
301 TGAAAATGAA GGCMAAAGG AGATCCACCT TCTACTTTCA TAAAGTTTCT ATCTTCTCT
ACTTTTACTT CCGTTTTTCC TCTAGGTGGA AGATGAAAGT ATTTCAAAGA TAGAAGGAGA
361 GCTGACTCAA ATAAGCATTT AATACATTTT ATAACGAATT AATTATGAAT ATATTTCAAA
CGACTGAGTT TATTGCTAAA TTATGTAAA TATTGCTTAA TTAATACTTA TATAAAGTTT
421 TAAATAAATT ATTTCCAAGT GTTGAAGGAA ATTCAGACTT CTAATTGCT CTGATTCTGA
ATTTATTAA TAAAGGTCA CAACTTCTCTT TAAGTCTGAA GATTAAACGA GACTAAGACT

108/130

FIG. 73B

481 AACTAAACA AATGCTCTGT GAGAGTTTGC GTTCCAGTG AAGTAGCGTG AGAATCCAA
TTGATTTTGT TTACGAGACA CTCTCAAACG CAAAGGTCAC TTCATCGCAC TCTTAGGTT

541 GTCAGACAGC TACATGAAC TACATTTACC AGCTCTCTGC CAGACACCAG TGCACGATAG
CAGTCTGTGG ATGTACTTTG ATGTAATGG TCGAGAGACG GTCTGTGGTC ACGTGTATC

601 CGCAGACAT GTAGCTAGAT CTCAGTCATA GCTNNNNNNN NNNNNNNNNN AGACCTTGCA
GCGTCTTGTA CATCGATCTA GAGTCAGTAT CGANNNNNNN NNNNNNNNNN TCTGGNACGT

661 GTTGGCTTTT AACCTGAAGG AGATAAGGCA AGATTCCAGG GTTTATTAG AGAATTACA
CAACCGAAAA TTGGACTTCC TCTATTCCGT TCTAAGGTCC CAAATAAATC TCTTTAATGT

721 GGATCTGGGA ATAAAGTAGT TACAAATTA GTCCCAACC AGCTTTCATG GAGCTTTCAA
CCTAGACCCT TATTTCATCA ATGTTTAAAT CAGGGGTTGG TCGAAAGTAC CTCGAAAGTT

109/130

FIG. 73C

781 TTATTAAATTA TTCTAGTTCT TAATCGGCAIG CATACAATGC ACAIACATAT ATACATGCAAT
AATAATTAAT AAGATCAAGA ATTAGCGTAC GTATGTTACG TGTATGTATA TATGTACGTA

841 ATTAATAATAC ATGATGGAC GCAAAACGGA ATAAGATTCC ACCTGTGCAT AAAACAGAAA
TAATTTTATG TACTAACCTG CGTTGGCCTT TATTCTAAGG TGGACACGTA TTTTGTCTTT

901 GACTTGGTTA GAGTGAGGGA TCAGGAACA CACACTGAG GACGAGATGN NNNNNNNNN
CTGAACCAAT CTCACTCCCT AGTCCTTTGT GGTGTGACTC CTGCTCTACN NNNNNNNNN

961 NTAGTGGGTG GGGGGGGGAC ATCAATAAAG AACTCTTCTG TGTACGCCAC TGAGCACGGA
NATCACCCAC CCCCCGCTG TAGTTATTC TTGAGAAAGAC ACAGTCGGTG ACTCGTGCCT

1021 ATAAAGGGAT GAGAGTGAGG GCAANTACCA GAAGATAAA ATCCTTTTAA GAGATGAAGA
TATTTCCCTA CTCTCACTCC CGTNNATGGT CTCTTTATTT TAGGAAAAAT CTCTACTTCT

1081 TTGTTATGAG CACAGTGTGT GNTTCAAAA ATCTTTTAAAC AACCCCAAGG TGAAGCTAGT
AACAAATCTC GTGTCAACACA CCNAAGTTT TAGAAAATTG TTGGGGTTC ACITCGATCA

1141 TGGAAAGATAT TTGAATTGT TTAACCCAT CTGGTCCTAG CCCTATTCTT TGAATCCCGA
ACCTTCTATA AACTTAACA AATTGGGTA GACCAGGATC GGGATAAGAA ACITAGGGCT

110/130

FIG. 73D

1201 AAGAGGGTCA AGAATTCCGA GCAGGAGTGG ACTACCTGGT GATACCTTAG ACTAGTCCTG
TTCTCCCACT TCTTAAGGCT COTCCTCACC TGATGGACCA CTATCGAATC TGATCAGGAC

1261 TGTATTAAAG TCCAATGAGG AGTATCTTGG TAAATATAATA AATAAGTCC CGAAATCCC
ACATAATTTC AGTTACTCC TCATAGAACC ATTATATTAT TTATTCAGG GCTTTTAGGG

1321 AGTACTGTGC TAGGAGATTI ACATGCTATA TIATTACTA TNNNNNNNT AATTGCAGA
TCATGACACG ATCCTCTAAA TGTACGATAT AATAAATGAT ANNNNNNNNA TTAAACGTCT

1381 TAATATTATC CTCATCATAA AATAGGGTAA CTAAGCTGA GAGGACTCG GTAACTTCTT
ATTATAATAG GAGTAGTATT TTATCCCATTT GATTGCGACT CTCCTGAGC CATTGAACAA

1441 CAAGGCCACT AAGAAGTGGC AAGTCAAAA CTGGAATTTT AATAAAGAG TCTAGCTTGC
GTTCCGGTGA TTCTTCACCG TTTCAGTTTT GACCTHAAA TTAATTTCTC AGATCGAAGC

1501 CTGTGTGGTT CTGCTTTTCT TAGAAAGTTG GANNAAGTCT CANATCAGTA CCCAGGAAA
GACACACCAA GACGAAAAGA ATCTTTCAC CTNNTTCAGA GTNTAGTCAT GGGTCTTTT

1561 ACAGCAAAAG ACCCGTGGT AAAGACCIGT CCAGATTGCT GACCTGGTTC ACACANHTCC

111/130

FIG. 73E

TGTCGTTTTC TGGGCGACCA TTCTCGGACA GGTCTAACGA CTGGACCAAG TGTGTNNAGG

1621 AAGCTTGCCT CTGTTACTTC CAAGGAAGAA AGAATGCACA GAGAGGTAAJ AAAACAACA
TTCGAACGGA GACAATGAAG GTTCCTTCTT TCTTACGCT CTCICCATTT TTTTGTTTGT

1681 AACCAACA AACAACA AACAACA AACAACA AACAACA AACTTCCTC
TTGGTTTGT TTGTTTGT TTGTTTGT TTGTTTGT TTGTTTGT TTGTAAGGAG

1741 TGTCTTGCAG GGCTCCAGCA CTTGGAACCT TCCTACGTCC TANTTTCAGG TTCTCTCAGT
ACAGAACGTC CCGAGGTCGT GAACTTGA AGGATGCAGG ATNAAAGTCC AAGACAGTCA

1801 TCTACCCCTCA ACCTGAGTGA CTGTCCTACC AGCAGCTTGT CGAGAACTCA GCCCTGCACC
AGATGGGAGT TGGACTCACT GACAGGATGG TCGTCGAACA GCTCTTGAGT CGGACGCTGG

1861 GTTCCCAGCT ACCCTCCTCC TAACTCGAGG GGTGCT
CAAGGGTCCA TGGGAGGAGG ATTGAGCTCC CCACGA

112/130

FIG. 74A

1 GGATTCGTGTT GAGCCCTAGC TCATTATGAT GTCCTGTTGT CCTACCCAAA TAAGACTCAT
CCTAAGACAA CTCGGGATCG AGTAATACTA CAGGACACA GATGGGTTT ATTCTGAGTA

61 CCCAACTACA TCTCAATAAT TAATGAAGAT GGAATGAGG TAAATAATAA ATAAATAAAT
GGGTGATGT AGAGTTATTA ATTACTCTA CCTTACTCC ATTTTATTT TATTATTTA

121 AAAAGAMACA TTCCCCCCA TTTATTATTT TTTCAAATAC CTTCATGAA ATAATGTTCT
TTTCTTTTGT AAGGGGGGT AATAATAAA AAAGTTATG GAAGTACTT TATTACAAAG

181 ATCCCTCTCT AATATTAAT AGAATCAAT ATTATTGGAA CTGTGAATAC CTTAAATATC
TAGGGAGAGA TTTATAATTA TCTTAGTTA TAATAACCTT GACACTTATG GAAATTATAG

241 TCATTATCCG GTGTCAACIA CTTTCCTATG ATGTTGAGTT ACTGGGTTA GAAGTCGGGA
AGTAATAGSC CACAGTTGAT GAAAGCATAC TACAACCTCA TGACCCCAAT CTCAGGCCCT

301 AATAATGCTG TAAANNNNN AGTTAGTCTA CACACCAATA TCAATAATGA TATACTTGT
TTATTACGAC ATTTNNNNN TCAATCAGAT GTGTGTTAT AGTTTATCT ATATGAACAT

361 AACCTCCAAG CATAAAAGA GATACTTAT AAAGAGGTT CTTTTTCT TTTTTTTT
TTGGAGGTTT GTATTTTCT CTATGAAATA TTTCTCCAA GAAAAAAGA AAAAAAAA

113/130

FIG. 74B

421 TCCAGATGGA GTTTCACCTCC TGTCAGGCCAG GCNGAGTGCA GTGGTGCCAT CTCGGCTCAC
AGTCTACCT CAAAGTGAGG ACAGTCCGTC CGNCTCAGGT CACCACGGTA GAGCCGAGTG

481 TGCACCTCC ACCTCCCATG TTCAAGGGAT TCTCCTCCT CAGTCTCCTG AGTAGCTGGG
ACGTTGGAGG TGGAGGGTAC AGTTCCTTA AGAGGAGGA GTCAGAGGAC TCATCGACCC

541 ATTACAGGTG TGCACCAACA CACCCAGCTA ATTTTGTAT TTTTAATAGA GACAGGGTTT
TAATGTCCAC ACOTGGTGGT GTGGGTGGAT TAAACACATA AAATTATCT CTGTCCCAAA

601 CATCGATGTT GCCCAGGCTA GTCTCGAACT CCTGACCTCT AGGIGATCCA CCCGCTCAG
GTAGCTACAA CCGGTCCGAT CAGAOCCTGA GGA CTGGAGA TCCACTAGGT GGGCGGAGTC

661 CCTCCCAAG TTGTAGAAIT ACACGTGTGA GGCACGTGCTC TGCCCAGGAG ATACATTTT
GGAGGGTTTC AACATCTTAA TGTGCACACT CCGTGACGAG ACCGCTCCTC TATGTAAAAA

721 GATAGGTTTA ATTTATAAG AACTGCACA GATTGCACT TCTGGGAAA TCACGATCCA
CTATCCAAAT TAAATATTTC TGTGACGTGT CTAAACCTCA ACCACCTTT AGTGCTAGGT

114/130

FIG. 74C

781 GTATGCCATTT GACCCAGCAA TTTTATTGG TACTTAATGA TTATATCTCA ATTGATCAGG
CATACGTAAA CTGGGTCGTT AAAAATAACC ATGAATTACT AATATAAGT TAACTAGTCC

841 TTGAACCTCG TCGGAGAAAT TTGTGTGGG ACATTGTAGA GGACAGTTTG GAGGCAAGGT
AACTTGAGAC ACGCTTCTTA AACACACACC GTAAACTCT CCGTCAAAAC CTCGGTTCCA

901 ATTTTAGTAG ATTAAAGAA TTTGAATCTT GTTGCAGT TGGGCATAT ACTGAGAAAG
TAAANTCATC TAAATTCTT AAACCTTAGA CAAACGTTCA ACCCGTATA TGACTCTTTC

961 AGAAGACAAT GCAGATAAAT TGATATATTT ATTATGATGT ATGTTCAATA TGAAGATCA
TCCTCTGTTA CGTCTATTTA ACTATATAAA TAATACTACA TACAAGTTAT ACTTCTAAT

1021 CAAAATATAA CATACATNNA TCTTACTTAA CATACCTCAG TTTTAGAGGT ACCGTATGTA
GTTTATATTT GTATGTANNT AGAATGAATT GTATGGAGTC AAATCTCGA TGGCATACAT

1081 GAAGAGTCCA TTCTATTTA GGTNAGTTCC TTTAGTCCTT TTATTACTGG GCACTCTTAA
CTTCTCAGGT AAAGATTAAT CCATTCAAGG AAATCAGGAA AATAIGACC CGTGAGAAAT

1141 TTACATGTAG CTTGAATAT GTCCAGTTG AGCAGTGAAC TGAATATGTC ATGTGATTAA
AATGTACATC GAACCTTATA CAGGTCAAAC TCGTCACCTG ACTTTTACAG TACACTAATT

1201 GTACATATAT AATTTTTTT CATAGTAGGT CAATAACCTC CTTTATTGA CTAAATGATC
CATGTATATA TTAAAAAAA GTAATATCCA GTTATTGGAG GAAATAAAT GATTACTTAG

1261 AGTCTCTAA TGATTATAG
TCAAGAGATT ACTAATATGC

115/130

FIG. 75A

10 20 30 40 50 60
1 AATCAAAATA AACAGTTAA AGTTTGATTA CTATAATCAA ACACAAAATA AATGAATATT
TTAGTTTAT TTTGTCAATT TCAAACTAAT CATATTAGTT TGTGTTTTTT TTAATTATAA
61 ATCTTTTATG TCAGTAGAGG GTGATGAAT CCTCAGGAT TTTGATGATA GTATCAGATA
TAGAAATAC AGTCATCTCC CACTTACTTA GGAAGTCCTA AAACACTATAT CATAGTCTAT
121 CCCAGCACTA TGCTAGAAGT TGTGAAGAT TCACGAGATG AATAAATCAC AGATTCTGTC
GGTCTGTGAT ACGATCTTCA ACACCTTCTTA AGTCTCTAC TTATTTAGTG TCTAAGACAG
181 CTCAAAATGG TTAGATCTAT TCAGGAACA AAGCTAAAA AACCCACCA ATAACTAAAA
GAGTTTACC AATCTAGATA AGTCCTTTGT TTCGATTTTT TTGGGGTGGT TATTGATTTT
241 ATCAACCAAA TGAAAAACAA CAATCATAAA ATAAGTAAGT ACCTATAGAA AGAAAGCTC
TAGTTGGTTT ACTTTTGTGTT GITAGTATTT TATTCATTCA TGGATATCTT TCTTTTCGAG
301 AGAGGAGGTA AAAAGATAAC TCTTCCAAA GGAATACTAT ATACTGTAAA CTGTGTACTG
TCTCCTCCAT TTTTCTATIG AGAAGGTTTT CCTTATGATA TATGACATTT GACACATGAC
361 ATAGAAGGAA GAATTAGAAA NNNNNNNNTG TAAGTGGCAT ACATACTAAG CTAAGTGTGAA
TATCTTCCCTT CTTAATCTTT NNNNNNNNAC ATTACCCGTA TGTATGATTC GATCACACTT

116/130

FIG. 75B

421 CACAAGCCTA AATATGTAGT TGCTTCACAG AAGTTAGAA GTAAATTAAC CTCATGAATT
GTGTTGGAT TTATACATCA ACGAAGTGC TTCCAATCTT CATTAAATTG GAGTACTTAA

481 TCTTGAGAGA ACTTGTAAGG ACTAAGCTTT CGATTTTGGG GAAAGATTTT AATACCAAAAT
AGAACTCTCT TGAACATTC TGAATCGAAA GCIAAAACCT CTTTCTAATA TTATGGTTTA

541 AAAAAGTACC TTTGTTTGGT AATCTCAATC ATTATAATAG TGCTTAGATA ATACCTAGGA
TTTTTCATGG AAACAAACCA TTAGAGTTAG TAATATTATC ACGAATCTAT TATGGATCCT

601 ACAAAATTA AATTAAATTT ACTTTAAAAA AAGTACATG ATTGGGGAAT CACAACCTGGC
TGTTTAATTT AATAATTAA TGAATTTTTT TTTCATGTAC TAACCCCTTA GTGTTGACCG

661 CTTACTAGAT TCTCTNNNNN NATATGCACT GAAAGAATG AAAAACACTG AACCAATAT
GAATGATCTA AGAGANNNNN NTATACGTGA CTTTCTTAC TTTTGTGAC TTGGTTTATA

721 NIGTTTTTTT AAGTTTAAAA TTAAATTGGA AAAAATAGT AAGGAATATC AGAAGCAAAA
NACAAAAAAA TTCAAATTTT AATTAACTT TTTTATATCA TTCCTTATAG TCTTCGTTTT

117/130

FIG. 75C

781 AAATAAAATG AAAGCAAGAA TCCTCAGAGG TAGCAGGAAA TTGGCTTTG CTTAGATGGA
TTTATTTTAC TTTCGTTCTT AGGAGTCTCC ATCGTGCTTT AAACCGAAAC GAATCTACCT

841 TCTATCAAAAG CTATGGCCCA TGAAAAGGAT TCAGGAGTTA GTTTAAAGCT GGTTACACATA
AGATAGTTTC GATACCGGGT ACTTTTCCTA AGTCCTCAAT CAAATTTCGA CCAAGTGTAT

901 ATGGAATCTA GCAGAAAGCT GTGCATAAAG GTGGTCTAAG AACAAACATA TCCTGACCCAG
TACCTTAGAT CGTCTTCTGA CAGGTATTTC CACCAGATTTC TTGTTGTTAT AGGACTGGTC

961 GTGAGGGGCG TCACNCTNAA TNCCAGCACT TTGGGAGCCC AAGGTGGGTG GATCAGGAGG
CACTCCCCCG AGTNGANTT ANGTCGTGA AACCTCGGG TTCCACCCAC CTAGTGCTCC

1021 TCAGGAGTTT GAGACCAGCC TGACCAACAT GGTGAACCG CGTCTCTACT AAAAATAGAA
AGTCCTCAAA CTCTGGTCGG ACTGGTTGTA CCACTTGGC GCAGAGATGA TTTTATCTTT

1081 AAATTAGCCG NGCCTACGTG CTTCTAATCC CAGCTGAACT CAGGAGACTG AGACAGGAGA
TTTAATCGGC NCGGATGCAC GAAGATTAGG GTCGACTTGA GTCCTCTGAC TCTGTCCTCT

1141 ATCACTTGAA CCCAGCATGC AAGCTTNNNN NNGCCACTGC ACTCCAGCCT AGGGTGCAAA
TAGTGAACCT GGGTCGTACG TTCGAANNNN NNCGGTGACG TGAGGTCCGA TCCACGTTT

1201 AAAAAAANA ANGACACATT ACTCAGGTAA GGTAATCAAT AA
TTTTTTTTT TNCGTGTAA TGAGTCCATT CCATTAGTAA TT

118/130

FIG. 76A

- AAGGTA AAAAATTATCTCTTTTTTTCTCTCCCCCAATGTAAAAAGTTATAG -
 - AAGGTA AAAAATTATCTCTTTTTTTCTCTCCCCCAATGTAAAAAGTTATAG -
 - TGGGTTTTACATGTGTAGAATCATTTTCTTAAAACTTTATGAATACCATT -
 - TGGGTTTTACATGTGTAGAATCATTTTCTTAAAACTTTATGAATACCATT -
 - ATTTTCTTGTTATTCTGTGACATGCCCACCTTACAGAGAGGACACATTTAC -
 - ATTTTCTTGTTATTCTGTGACATGCCCACCTTACAGAGAGGACACATTTAC -
 - TAGGTTATATCCCGGGGTTAAATTCGAGCATTGGAATTTGGCCAGTGTAG -
 - TAGGTTATATCCCGGGGTTAAATTCGAGCATTGGAATTTGGCCAGTGTAG -
 - ATGTTTAGAGTGAACAGAACA AATTTTTCTGTGCTTACAGGTTATGGCTG -
 - ATGTTTAGAGTGAACAGAACA AATTTTTCTGTGCTTACAGGTTATGGCTG -
 - TGGCCTACAAGAAGCATGCACTGGGTTTATTATTAACTTTCA GTATCTTT -
 - TGGCCTACAAGAAGCATGCACTGGGTTTATTATTAACTTTCA GTATCTTT -
 - GTTTTAAATATTTTCTACAAAAATGTTTACTAAATTAAATTG TAGTATGA -
 - GTTTTAAATATTTTCTACAAAAATGTTTACTAAATTAAATTG TAGTATGA -
 - ATTGTTATAAATAATGAGGGAAAA CAATTTACACATAGCAAATTTAAAAA -
 - ATTGTTATAAATAATGAGGGAAAA CAATTTACACATAGCAAATTTAAAAA -
 - TTAGTGTCATTTGATTTGTTAATATATTTTTCTCTTTAGTGGGAAATTAA -
 - TTAGTGTCATTTGATTTGTTAATATATTTTTCTCTTTAGTGGGAAATTAA -
 - ATTTTAAAAAATTCCCTTTTCGACTGTAGAACA AATAGGAATTTGGCCTGT -

119/130

FIG. 76B

```
|||||
- ATTTTAAAAAATTCCCTTTGACTGCTAGAACAAATAGGAATTTGGCCTGT -
|||||
- GGGGTCTACTTGCTTATTATATTTGTAAGCTAGTGGTAGGAAATAGCAA -
|||||
- GGGGTCTACTTGCTTATTATATTTGTAAGCTAGTGGTAGGAAATAGCAA -
|||||
- TGCTCACTACCACTAATAAGAACATTTCTAAATCTGATGTTCTGAGGATT -
|||||
- TGCTCACTACCACTAATAAGAACATTTCTAAATCTGATGTTCTGAGGATT -
|||||
- TTTAGAGCTTATAGTAGCAAAAAGAAAAGGGAAATTCTATCCGAGATGTC -
|||||
- TTTAGAGCTTATAGTAGCAAAAAGAAAAGGGAAATTCTATCCGAGATGTC -
|||||
- CTTTGTTGTAGGCCTAATGAGAAAAGGTTGAAGATAAAGTTCTGGTACTC -
|||||
- CTTTGTTGTAGGCCTAATGAGAAAAGGTTGAAGATAAAGTTCTGGTACTC -
|||||
- ATTTAAGTGTAATATTGAAAATTGATATTACCGAATCTGGAACAACCAAT -
|||||
- ATTTAAGTGTAATATTGAAAATTGATATTACCGAATCTGGAACAACCAAT -
|||||
- TTAAAATAAGGAAAGAAAGACACTGTGTTTTCT -
|||||
- TTAAAATAAGGAAAGAAAGACACTGTGTTTTCT -
```

120/130

FIG. 77A

10	20	30	40	50	60	
1	AGAAAACACA	GTGTCCTTCT	TTCCCTTAATT	TAAATTGGTT	GTCCAGATT	CGGTAATATC
	TCCTTTGTGT	CACAGAAAGA	AAGGAATAAA	ATTAAACCAA	CAAGGTCTAA	GCCATTATAG
61	AATTTCAAT	ATTACACTTA	AATGAGTACC	AGAACTTTAT	CTTCAACCTT	TTCTCATTAG
	TTAAAAGTTA	TAATGTGAAT	TTACTCATGG	TCTTGAATA	GAAGTTGGA	AAGAGTAATC
121	GCCTACAACA	AAGGACATCT	CGGATAGAAT	TTCCCTTTTC	TTTTTGCTAC	TATAAGCTCT
	CGGATGTTGT	TTCCCTGTAGA	GCCTATCTTA	AAGGMAAAG	AAAAACGATG	ATATTCCGAGA
181	AAAAATCCTC	AGAACATCAG	ATTAGAAAT	GTTCTTATTA	GTGGTAGTGA	GCATTTGCTA
	TTTTTAGGAG	TCTTGTAGTC	TAAATCTTTA	CAAGAATAAT	CACCATCACT	CGTAAACGAT
241	TTTCCTACCA	CTAGCTTACA	AATATAATAA	GCAAGTAGAC	CCCACAGGCC	AAATTCCTAT
	AAAGGATGGT	GATCGAATGT	TTATATTATT	CGTTCATCTG	GGGTGTCCGG	TTTAAGGATA
301	TTGTTCTACA	GTCGAAAGGG	AATTTTTTAA	AATTTAATTT	CCCACATAAG	AGAAAATAT
	AACAAGATGT	CAGCTTTCCC	TTAAAAAATT	TTAAATTAAA	GGGTGATTTC	TCTTTTATA
361	ATTAACAAAT	CAAATGACAG	TAATTTTTAA	ATTGCTATG	TGTAANTTGT	TTTCCCTCAT
	TAATTGTTTA	GTTTACTGTC	ATTAAAAATT	TAAACGATAC	ACATTTAACA	AAAGGGAGTA
421	TATTATAAC	AATTCATACT	ACAATTTAAT	TTAGTAAACA	TTTTTGTAGA	AAATATTTAA
	ATAAATATTG	TTAAGTATGA	TGTTAAATTA	AATCAATTGT	AAAAACATCT	TTTATAAATT

121/130

FIG. 77B

481 AACAAAGATA CTGAAAGTTA ATATNAAACC CAGTGCATGC TTCITGTAGG CCACAGCCAT
TTGTTTCTAT GACTTTCAAT TATANTTTGG GTCACGTACG AAGRACATCC GGTGTCGGTA

541 AACCTGTAAG CACAGAAJAA TTTGTTCTGT TACTCTNAAAC ATCTACACIG GCCAAATTCC
TTGGACATTG GTGTCTTTT AAACAAGACA ATGAGATTGG TAGATGTGAC CGGTTTAAAGG

601 AATGCTCGAA TTTAAACCCG GGATAAACC TAGTAATGT GTCCTCTCTG TAAGGTGGGC
TTACGAGCTT AAATTGGGGC CCTATATTGG ATCAATTACA CAGGAGAGAC ATTCCACCCG

661 ATGTCACAGA ATACAAGAA ATAATGGTAT TCATAAAGTT TTAAGAAAT GATTCTACAC
TACAGTGTCT TATGTTCTT TATTACCATA AGTAITTCAA AATCTTTTA CTAAGATGTG

721 ATGTAAACC CACTATAACT TTTTACATTG GGGGAGAGAA AAAAGAGAT AATTTTACC
TACATTTTGG GTGATATTGA AAAATGIAAC CCCCTCTCTT TTTTCTCTA TTAATAATGG

781 TT
AA

122/130

FIG. 78A

10 20 30 40 50 60
1 GATGCTATTT GGGCAATTTC TTATTGACAG TTTTGAATG TTAGGCTTTT ATCTCCATT
CTACGATAAA CCGTTAAAG AATAACTGTC AAACITTTAC AATCCGAAAA TAGAGGTAAA
61 TTTAGTACTT AAATTTTCCA ACATGGGTGT TGCTTGTAT TTTATCAGTA TAAATAGAA
AAATCATGAA TTTAAAGGT TGTACCCACA ACGAACAAATA AAATAGTCAT ATTTATCTT
121 GAGTGGTTCT GTTCTGGAAT TTAGTATATA CATGAGTATC TAGTGATGT CAGCCATGAA
CTCACCAAGA CAAGACCTTA AATCATATAT GTACTCATAG ATCACATACA GTCGGTACTT
181 AATGAACCTT TCAGATGTTT AACTTCAGGG AACCTAATTG AGTCATTGCT CCAGACATTG
TTACTTGGA AGTCTACAAA TTGAAGTCCC TTGGATTAA TCAGTAACGA GGTCTGTAAC
241 TTGCTTTGAA CCCACTATAT TNNNNNNNCT CGGGCAATGA CTCAGTGTGG CAAGGATACT
AACGAAACTT GGGTGATATA ANNNNNNNGA GCCCGTTACT GAGTCACACC GTTCCTATGA
301 ACTGCAGGCC TGTCTCTGGA AGGCACIGGA CTCCTCTGAT GCAAACCTTG GCCAGGGACT
TGACGTCCGG ACAPAGACCT TCCGTGACCT GAGGAGACTA CGTTTGAAAC CGGTCCCTGA
361 CCTTGATAGC TCTTAAATAG ATGCTGCACC AACACTCTCT TTCTTTTCTC TCTTTTCTT
GGAACATATCG AGAATTATC TACGACGTGG TTGTGAGAGA AAGAAAGAG AGAAAAAGAA

123/130

FIG. 78B

421 TATTCAATAT TAGACTACAA GCAGTCTNAG GACTTCTCAG GGTTCCTAGC TCTCTCTCAT
ATAAGTTATA ATCTGATGTT CGTCAGATTG CTGAGAGTGC CCAAGATCG AGAGAGAGTA

481 TTCACACATG CTTTCCTAGT AATCTCTACT CAIATATCTT ACTGCTACGC TGGGGCCAGA
AAGTGTGTAC GAAAGGATCA TTAGAGATGA GTATATAGAA TGACGATGCG ACCCCGGTCT

541 TAACNNNNNN CTTCCATTTT GTTTTATCTT CTATTCITCI TCCCCTTCTG CTTTCATTAT
ATTGNNNNNN GAAGGTAAA CAAAATAGA GATAAGAAGA AGGGGAAGAC GAAAGTAATA

601 TGAACCTTC TGCTTTCATT ATTGAAACTT TCCCAGATTT GTTCTGCTTA ACCTGGCATT
ACTTTGAAG ACGAAAGTAA TAACTTTGAA AGGTCTAAA CAAGACGAAT TGGACCGTAA

661 GGAAC TGTTT CCTCTCCCT GTGCTGCTTT CTCCCATGCG CATGTCCTTT TTTTTTTTTT
CCTTGACAAA GGAGAAGGGA CACGACGAAA GAGGTTAAG GTACAGGAAA AAAAAAAAAA

721 TTTTTTTTTT TGAGACAGTG TCACTCTGTT GCCCAGGCTG GAGTGCAATG GTGCAATCTT
AAAAAAAAAA ACTCTGTCAC AGTGAGACAA CGGGTCCGAC CTCACGTTAC CACGTTAGAA

124/130

FIG. 78C

781 GCCCACTGCA ACCCCGCGCT CCCGGGTTC AAGTATTCTC CTGCCTCAGC CTCTGAGTA
CCGGIGACGT TGGGGGCGGA GGGCCCAAGT TCACTAAGAG GACGGAGTCG GAGGACTCAT

841 GCTGGGATTA CAGGTGCCCC CCACTATGCC CGGCTGATT TTGTATTTT AGTAGAGATN
CGACCCTAAT GTCCACGGGT GGTGATACGG GCGGACTAAA AACATAAAA TCATCTCTAN

901 NNNNNNTTT CACCATNGCT GATCAGGCTG GTCTCGAACT CCTGACCGCA GTGANTCCGC
NNNNNNNAAA GTGGTANCGA CTAGTCCGAC CAGAGCTTGA GGAAGTGGGT CACTNAGGCG

961 CCTCCTTGGC CTCCCAGGT GCTGAGATTA CAGGCATGAG TCACTGCGNC CAUCCACCAT
GGAGGAACCG GAGGGTTTCA CGACTCTAAT GTCCGTACTC AGTGACGCG GTGCGTGCTA

1021 TATTCTCTAG AGGTGAGAGA ACACGTGGTC TTCTAACAG TTGAAATTG ATAGAGACC
ATAAGAGATC TCCACTCTCT TGTGACCGAG AAGATTGTT CACTTTAATC TATCTCTG

125/130

FIG. 79A

10	20	30	40	50	60	
1	CACAAAAA	GATTATTAGC	CACAAAAA	CCTTGAAGTA	ACGCATTAA	ATGTTAATGG
	GTGTTTTT	CTAATAATCG	GTGTTTTT	GGAATTICAT	TGCSTAATIT	TACAATTACC
61	ATTCACTTTA	TTGAGCATCT	GCTCATAATA	CTTTAATGAG	TGCAAGTGC	TTTGAATATA
	TAAGTGAAAT	AACTCGTAGA	CGAGTATTAT	GAAATTACTC	ACGTTTCACG	AAACTTATAT
121	ATACGTCATT	TAAACCTTAC	CATAATTCIG	AGGAATTGCT	ACCTCCACTT	CACAGATGGG
	TATGCAGTAA	ATTGGAATG	GTATTAAGAC	TCCTTAAACGA	TGGAGGTGAA	GTGTCATCCC
181	GCACAGGAGG	CTTAGATAAC	ATGCCCAAG	TCATGCTTCT	AGTAAATGGA	TATAATTAAAG
	CGTGTCCTCC	GAATCTATTG	TACGGGTTTC	AGTACGAAGA	TCATTTACCT	ATATTAAATTC
241	ATTCAAATTA	TTGATAAGAA	TTTGATCTGC	CTTACCAGTA	TCTAGTAGTA	AATCTAAAG
	TAAGTTTAAT	AACTATTCTT	AACTAGACG	GAAATGGTCAT	AGATCATCAT	TTAGATTTTC
301	CGCTTTCCAG	AGCATGTGCT	GTTGATAGAG	CTTGATGCT	AACTCTCTGA	AATTTTCCAT
	GCGAAAGGTC	TCGTACACGA	CAACTATCTC	GAACTACAGA	TTGAGAGACT	TTAAAGGTA
361	TCTTATTGT	CTCACTGGTA	TATAGTTATT	TTTTACTACT	TTCATACACC	TACTAAGAG
	AGAATAARCA	GAGTGACCAT	ATATCAATAA	AAATGATGA	AAGTATGTGG	ATGATTTCTTC

126/130

FIG. 79B

421 ACAGGAGGAT CAAAGATAGG ATTTCATTTA GAATGCCCTAA AGCTTCACGT ATTTAAATTC
TGTCCTCCTA GTTTCATATCC TAAAGTAAAT CTTACGGATT TCGAAGTGCA TAAATTTAAG

481 AGAATAAGAT TCAGGCCAGAC CACCAGTATA TGCCATGGTC CCTGGTTATC TTTCAGCAGG
TCTTATTCTA AGICCGTCTG GTGGTCATAT ACGGTACCAG GGACCAATAG AAAGTCGTCC

541 TGACCCGAGAA AGAAACATG GTAATGTITA TGAATGCTG GGTCTTGTGTA GTTTCACCTC
ACTGGCTCTT TCTTTGTGAC CATTACAAAT ACTTIACCAC CCAAGAACAT CAAAGTGAAG

601 AACATACTG CCTTTACIGT ATTAAGATGA TGGATTAACT TATCTTGAT ATGGGCATGT
TTGTATAGAC GGAATGACA TAATCTACT ACCTAATTGA ATAAGAACTA TACCCGTACA

661 AAACAATAT ACTTTTACTA AACAGCTACA GAGAGACAAA TGTGTTTCCA GACAAACTTA
TTTTGTATA TGAAATGAT TTGTCGATGT CTCTCTGTTT ACACAAAGGT CTGTTTGAAT

721 AGAGACTGAG TGTTCAACT GAATAATCTC GACCTTAATT GTAACATAT TTAATGAAAT
TCTCTGACTC ACAAGTTTGA CTTATTAGAG CTGGAATTAA CATTGATATA AAATACTTTA

127/130

FIG. 79C

781 CCAGCTGTAA GGC AAAACA GACTTCTTTG GGCTACCAC GGGCATTTTG TTCTGTAN
GGTCGACATT CCGTTTTTGT CTGAAGAAC CCGATGGTG CCGTAAAC AGGACAATN

841 NNNTACTCCA AACCTTAAC CCACGTCCAC TTAAATRAIG GCCTGGAAAT AAATGTCATT
NNNATGAGGT TTGGAATTG GGTGCAGGTG AATTATTAC CGACCTTTA TTACAGTAA

901 ATCIGATATT ATACTGAGAT GTTAGTTAT GAATCAAA GTGGAGAAT TCAATCTGTC
TAGACTATAA TATGACTCTA CAAACNATA CTTAGTTTT CACCTCTAA AGTTAGACAG

961 CTGTAAGCTT TCTCTGGGT CACGACCCIC ATGCACTCAG GCTGTGCGGT GCAGCATGCT
GACATTGAA AGAGACGCCA GTGCTGGAG TAGGTGAGTC CGACACGCCA CGTCGTACGA

1021 CTGTCATGTC TGTCTCTTC TGCCTGTACA CGGGTGGTTG TTCCTGTCTA CCTGTTTGAG
GACAGTACAG ACNAAAGAAG ACGACATGT GCCCACC AACAGCAGAT GGACAACTC

1081 GAAATATGAA TACGTNNNN NCTAGAATCT ACTGCACATG CAATAAGGAA ACAATCAGTA
CTTTATACTT ATGCANNNNN NGATCTTAGA TGACGTGTAC GTTATTCCTT TGTAGTCAT

1141 AGAATCACTT TCTCGTGGAA AATTCATTAG AATTAACATC TCGTTTTAAA ATGCTCTATC
TCTTAGTGAA ACAGCACCTT TTAAGTAATC TTAATTGTAG AGCAAAATTT TACGAGATAG

128/130

FIG. 79D

1201 AAAGTGTAAG TAATTCCTCT CTCCTTTCCC TTTTCACTA AGGAGTTTGT ATATTAACA
TTTCACATTT ATTAAGGAGA GAGAAAAGG AAAAGTGAT TCCTCAAACA TATAATTGT

1261 GAATTCAAG TAATGTATTA TAAATTTATT TAANNATTT ACAATAAAT GCCACGTATA
CTTAAAGTTC ATTACATAAT ATTTAAATAA ATNNATAAA TGTATTTTA CCGTGCAAT

1321 AGCATCAAGC AACATGANN NNNCATTTGT AGAAGCACA ATACATAGTC AAAACAGCAG
TCGTAGTTTG TTGTACTIONN NNGTAACCA TCTTTCGTGT TATGTATCAG TTTTGTGTC

1381 AGTATTAAAT AACACAGAAA TTTGCAAAAG GCAAGTAAAG AATATACATA TACTTAATTA
TCATAATTTA TTTGTCTTTT AAACGTTTTC CTTTCATTTC TTATATGTAT ATGAATTAAT

1441 TACATAAAAT ATTGATACAG GAGGTAGAAA GAAATTTAGT AAGCAGATAA TGGGGGCAAC
ATGTATTTTA TAACTATGTC CTCATCTTT CTTTAAATCA TTCGTCTATT ACCCCCCTTG

1501 AGAGTCCTCA GCAGAGCTTC CCTTCTAACA AAAAGCAGCC CAATAAATTA TTTTTTTTTT
TCTCAGGAGT CGTCTCGAAG GGAAGATTGT TTTTGTGTCGG GTTATTTAAT AAAAAA

1561 CTAACAAAA GCAGCCCTGAA AATCGAGCI GCAACATAG ATTAGCAATC GGCTGAAAGT

129/130

FIG. 79E

GATTGTTTTT CGTCGGACTT TTTAGCTCGA CGTTTGTATC TAATCGTTAG CCGACTTTCA

1621 GCGGGAGAAT GCTGGCAGCT GTGCCAATAG TAAAGGGCIA CCTGGAGCCG GCGCGGTGGC
CGCCCTCTTA CGACCGTCGA CACGGTTATC ATTCCCGAT GGACCTCGGC CCGCGCACCG

1681 TCACGCTGTA ATCCAGCAC TTTGGGAGGG CGAGGCAACG CGATCACCT GAGTCCGGA
AGTGGGACAT TAGGGTCGTG AAACCTCCC GCTCCGTTGC GCCTAGTGGA CTCCAGCCCT

1741 GTTTGAGATC AGCCCGACCA ACATGGAGAA ACCCGTCTC TACTAATAAA AAAAAAAAA
CAAACTCTAG TCGGGCTGGT TGTACCTCTT TGGGGCAGAG ATGATTTTTT TTTTTTTTTT

1801 AAAGGCAAAA AATGAGCCGG GCATGGTGGC ACATGCCCTG CACATCCCAG CTGAGGCAGG
TTTCCGTTTT TTAATCGGCC CGTACCACCG TGTAGGGAAC GTGTAGGTC GACTCCGTCC

1861 AGAATTCACT TGAACCTGGG AGGTAGAGAT TCGGTGAAG CGAGATCAG TCATTGCCACT
TCTTAAGTGA ACTTGGACCC TCCATCTCTA AGCCCACTC GCTCTAGTGC AGTAACGTGA

1921 CCAGCCTGGG CAAAAGAGC AAACCTAGT CTCAAAAAA AAAAAAAAA GAAAAA
GGTCGGACCC GTTTTCTCG TTTTGAATCA GAGTTTTTT TTTTNGTTT CTTTTT

130/130

FIG. 80

Genomic Organization of PSM Gene

